

High Throughput Multiplex DNA Sequence Amplifications

Reference to Government Grant

This invention is made with government support under grant R01-HG02094 awarded
5 by the National Human Genome Research Institute. The U.S. government may have certain
rights in this invention.

Field of the Invention

This invention pertains to the field of high throughput multiplex DNA sequence
amplification. Specifically, the invention pertains to methods of designing primers that allow
10 the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase
chain reaction and minimize the formation of nonspecific extension of undesired DNA
fragments.

Background

The polymerase chain reaction (PCR) is a primer-directed *in vitro* reaction for the
15 enzymatic amplification of a specific DNA fragment. Saiki, Enzymatic Amplification of β -
Actin Genomic Sequences and Restriction Site Analysis for Diagnosis of Sickle Cell Anemia,
Science 230: 1350-54 (1985). The PCR process is involved in the repetitive cycles of
denaturation, primer annealing and extension by a thermostable DNA polymerase of two
oligonucleotide primers that flank the DNA region of interest in a template DNA sample. At
20 the beginning the PCR process, the duplex DNA target is denatured into two separated
strands of DNA through a first heating step. In a subsequent annealing step, each
oligonucleotide primer anneals or hybridizes to the complementary sequence of one separated
strand of the target DNA. In a third extension step, nascent DNA is synthesized by extending

each primer from its 3' hydroxyl end of towards the 5' end of the annealed target DNA strand by a thermostable DNA polymerase. The heating or denaturation step, the primer annealing step and the enzymatic extension step together constitute a single PCR cycle. If the newly synthesized DNA strand extends to or beyond the region complementary to the other primer, it serves as a primer annealing site and a template for extension in a subsequent PCR cycle. As a result, the repetitive PCR cycles give rise to the exponential accumulation of a specific DNA fragment whose termini are defined by the 5' ends of the two primers. Theoretically, at the n th cycle of the PCR process, a single DNA molecule can produce 2^n progeny DNA fragments of interest.

The distinctive nature of the PCR process in producing a substantive quantity of DNA fragments of interest from an initial tiny amount of DNA sample has gained broad applications in the field of biomedical research and clinical diagnosis. For example, PCR has been widely used in the diagnosis of inherited disorder and the individualization of evidence samples in the forensics area. Erlich *et al*, Recent Advances in the Polymerase Chain Reaction, *Science* 252: 1643-51 (1991); Newton & Graham, PCR (Oxford, 1994). In particular, PCR has played a critical role in genotyping a vast number of genetic polymorphisms and individual variations which underlie the onset of many diseases. Shi, Enabling Large-Scale Pharmacogenetic Studies by High-throughput Mutation Detection and Genotyping Technologies, *Clin. Chem.* 47: 164-172 (2001).

Widespread applications notwithstanding, the use of PCR is quite often limited by cost, time, and the availability of adequate test samples. To illustrate, the human genome project has placed over 6000 DNA markers in human genetic mapping. To analysis these 6000 markers in 1000 specimens, a total of 6,000,000 PCR reactions are needed if only one

marker sequence is amplified in each reaction. As a well equipped laboratory may process 300 reactions and post-PCR assay a day, it will take a total of 20,000 working days or 80 years to complete the analysis, provided that the amount of each specimen suffices 6000 reactions.

5 In overcoming these limitations, a variant PCR termed multiplex PCR has been developed. Chamberlian *et al*, Deletion Screening of the Duchenne Muscular Dystrophy Locus via Multiplex DNA Amplification, *Nucleic Acids Res.* 16: 11141-56 (1988). Unlike the standard or uniplex PCR where only one pair of primers is used to amplify a single DNA fragment of interest, the multiplex PCR includes more than one pair of primers and thus
10 results in more than one DNA fragment. Since its inception, the multiplex PCR has been applied in many areas of DNA testing, including gene deletion analysis, Chamberlain, *supra*, mutation and polymorphism analysis, Rithidech *et al*, Combining Multiplex and Touch Down PCR to Screen Murine Microsatellite Polymorphism, *Bio-Techniques* 23: 36-45 (1997), quantitative analysis, Zimmermann *et al*, Quantitative Multiple Competitive PCR of HIV-
15 DNA in a Single Reaction Tube, *BioTechniques* 21: 480-484 (1996), RNA detection, Zou, Identification of New Influenza B virus Variants by Multiplex Reverse Transcription-PCR and the Heteroduplex Mobility Assay, *J. Clin. Microbiol.* 36: 1544-1548 (1998), and identification of microorganisms, Elnifro *et al*, Multiplex PCR: Optimization and Application in Diagnostic Virology, *Clin. Microbiol. Rev.* 13: 559-570 (2000).

20 Conceptually, the multiplex PCR has the potential to produce considerable savings in cost, time and sample volume. In aforementioned project of analyzing 6000 DNA markers in 1000 specimens, if n pairs of primers are used in a multiplex PCR reaction, it will only cost one- n th of 20,000 working days to complete the project as well as one- n th of the cost and

sample volume required in the uniplex PCR reactions. Despite the attractive potential, the application of the multiplex PCR poses many challenges. For example, even under carefully optimized reaction conditions, only 26 DNA fragments could be amplified simultaneously in a single multiplex PCR. Edwards & Gibbs, Multiplex PCR: Advantages, Developments and

5 Applications, *PCR Meth. Appl.* 3: S65-75 (1994); Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

Researchers are facing two tiers of challenge in optimizing the multiplex PCR. The first tier of challenge is the efficacy of PCR. In general, this issue is ubiquitous in all PCR
10 reactions, whether in multiplex PCR or uniplex PCR. The efficacy of PCR is measured by its specificity, efficiency and fidelity. A highly specific PCR will generate one and only one amplified DNA fragment of intended sequence from each pair of primers. More efficient amplification will generate more products with fewer PCR cycles. A high-fidelity PCR product has the minimal amount of DNA polymerase-induced errors. Studies have shown the
15 efficacy of PCR is affected by factors including the primer annealing temperature, the activity and concentration of the thermostable DNA polymerase, the PCR buffer components such as dNTPs and MgCl₂, and the first cycle set-up. Roux, Optimization and Troubleshooting in PCR, *PCR methods Appl.* 4: S185-S194 (1995); Roberston & Walsh-Weller, An Introduction to PCR Primer Design and Optimization of Amplification Reactions, *Methods Mol. Biol.* 98:
20 121-154 (1998). Special attention has also been paid to the primer parameters, such as homology of primers with their target DNA sequence, primer length, GC content, ratio of primers to the template DNA. Researchers are cautioned that the efficacy of PCR is often a delicate balance among specificity, efficiency and fidelity. Cha & Thilly, Specificity,

Efficiency, and fidelity of PCR, *PCR Methods. Appl.* 3: S18-S19 (1993). Adjusting the conditions for specificity may compromise the efficiency or fidelity and *vice versa*.

The second tier of challenge in multiplex PCR is the presence of multiple pairs of primers that are unique to multiplex PCR. It is reported that the presence of more than one primer pair increases the chance of obtaining spurious amplification products, primarily because of the formation of nonspecific DNA extensions, e.g., primer dimers. Markoulatos *et al*, Multiplex Polymerase Chain Reaction: A Practical Approach, *J. Clin. Lab. Anal.* 16: 47-51 (2002). The nonspecific extensions occur when 1) a first primer non-specifically interacts with a second primer because the first primer shares a certain degree of complementarity in its 3' sequence with the 3' sequence of the second primer; and 2) when a primer non-specifically interacts with a DNA sequence of a template DNA which is not the target DNA sequence. Elnifro, *supra*. The nonspecific extensions undermine not only the specificity of PCR but the efficiency as well. The nonspecific products compete with desired target DNA, consume the limited supplies of enzymes, primers and nucleotides, and produce impaired rates of annealing and extension. Markoulatos, *supra*. Not surprisingly, the non-specific extension limits the number of desired DNA fragments in a single multiplex PCR and poses a major limitation to the application and efficacy of multiplex PCR. Lin *et al*, Multiplex Genotype Determination at a Large Number of Gene Loci, *Proc. Natl. Acad. Sci. USA* 93: 2582-2587 (1996).

So far little progress has been made in combating the nonspecific extension problem. Researchers have developed a method to lower the chance of forming the nonspecific extension by adding a universal tail sequence to the 5' end of the sequence-specific primers.

Lin *et al, supra*; Brownie *et al*, The Elimination of Primer-Dimer Accumulation in PCR,

Nucleic Acids Res. 25: 3235-3241 (1997). The tailed primers are added in a multiplex PCR reaction at very low concentrations and allowed to participate the early cycles of reaction. In subsequent cycles, the primers complementary to the universal tail sequence are added into
5 the reaction at high concentrations and proceeded to continue PCR cycles. This method has reportedly produced 26 DNA fragments and minimized the accumulation of non-specific extensions. Lin *et al, supra*. However, the addition of a tail sequence does not thoroughly tackle the problem of non-specific interaction among primers or between a primer and a target DNA.

10 Thus, there is a need in the art to design primers that allow the simultaneous amplification of a multiplicity of DNA fragments in a single polymerase chain reaction. There is a need in the art to design primers that minimize or substantially reduce the formation of nonspecific extension of undesired DNA fragments. There is a need in the art to design primers that significantly enhance the efficacy of multiplex polymerase chain
15 reactions.

Brief Description of the Drawings

Fig. 1 is an illustration of five forms of primer-primer interactions.

Fig. 2 is an illustration of three forms of interactions between primers and nonspecific target templates.

20 Fig. 3 is an illustration of a genotyping microarray determining the genotypes of a DNA sample at the 627 loci.

Fig. 4 is an illustration of a set of criteria in designing primers that are experimentally acceptable.

Summary of the Invention

One aspect of the present invention relates to methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

In one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a first primer and a second primer or the first primer comprises the steps of aligning the first primer and the second primer and selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.
- 5) the maximal match between the first primer and the second primer does not exceed 75%.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a

template DNA comprises the steps of aligning the primer and the template DNA and selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and 2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer;
- 5) the first primer at its 3' end does not contain 15 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary;

6) the primer at its 3' end does not contain 18 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

7) the maximal match between the first primer and the second primer used in the multiplex amplification does not exceed 75%.

Another aspect of the present invention relates to computer products or computer programs which, once executed by a computer process, perform methods as disclosed in the present invention.

The methods according to the present invention increase the number of desired DNA fragments, enhance the efficacy of the multiplex PCR and achieve a significant reduction in cost, time and sample volume. A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments.

The methods according to the present invention significantly broaden the application of multiplex PCR in the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, the gene expression profiling in various samples, and high throughput genotyping technologies which include oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

Detailed Description of the Invention

The primary aspect of the present invention provides methods of designing PCR primers that allow the efficient and simultaneous amplification of a large number of different desired DNA fragments in a single multiplex PCR and minimize the formation of nonspecific extensions of undesired DNA fragments.

The nonspecific extension of unwanted DNA fragments is a major factor in preventing effective applications of multiplex PCR. The nonspecific extension is caused by nonspecific interactions between different molecules of either the same primer, or different primers, or a primer and a non-primer specific region of DNA templates. Specifically, the nonspecific interactions are caused by 1) a stretch of perfectly matched sequence at the 3' ends of two primers, 2) a stretch of perfectly matched sequence with only one mismatch at the 3' ends of two primers, 3) a stretch of the 3' end sequence of a primer perfectly matching to the internal sequence of the same primer, another primer, or a non-primer specific region of a DNA template, 4) a stretch of the 3' end sequence of a primer perfectly matching with only one mismatch to the internal sequence of itself, another primer, or a non-primer specific region of a DNA template, or 5) a stretch of a sequence in a primer matching to itself, another primer, or a non-primer specific region of a DNA template. Fig. 1. The nonspecific extensions of undesired DNA fragments compete and consume the same reagent components in the PCR reaction and thus impair the production and extension of desired DNA fragments. The problem of nonspecific extensions is aggravated when multiple pairs of primers of high concentrations are present in a single multiplex PCR.

One embodiment of the present invention circumvents the nonspecific extension by setting forth a list of criteria in designing PCR primers useful for multiplex PCR. According

to one embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and all the rest of primers including the primer comprises the steps of selecting a first primer wherein:

- 1) the first primer at its 3' end does not contain four or more bases that are
5 perfectly matching to the 3' end sequence of the first primer or a second primer;
- 2) the first primer at its 3' end does not contain seven or more bases that are perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;
- 3) the first primer at its 3' end does not contain six or more bases that are
10 perfectly matching to a sequence anywhere of the first primer or the second primer; and
- 4) the first primer at its 3' end does not contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer.

The same method repeatedly applies to the selection of a subsequent primer until all
15 the selected primers meet the above criteria.

According to another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions between a primer and a non primer-specific region of the a template DNA comprises the steps of selecting a primer wherein:

- 1) the primer at its 3' end does not contain 13 or more bases that are perfectly
20 matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

2) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

According to another embodiment of the invention, the method of designing primers to minimize the nonspecific extensions in a multiplex PCR comprises the steps of selecting a first primer wherein:

5 5) the first primer at its 3' end does not contain four or more bases that are perfectly matching to the 3' end sequence of the first primer or a second primer;

6) the first primer at its 3' end does not contain seven or more bases that are
10 perfectly matching except one mismatch to the 3' end sequence of the first primer or the second primer;

7) the first primer at its 3' end does not contain six or more bases that are perfectly matching to a sequence anywhere of the first primer or the second primer;

8) the first primer at its 3' end does not contain eleven or more bases that are
15 perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer,

9) the first primer at its 3' end does not contain 13 or more bases that are perfectly matching to any sequence of a DNA template other than the specific sequence to which the primer is complementary; and

20 10) the primer at its 3' end does not contain 17 or more bases that are perfectly matching except one mismatch to any sequence of a DNA template other than the specific sequence to which the primer is complementary.

In practicing the present invention, each primer to be used in a multiplex PCR is selected through the methods described herein. The selection of primers for a large number of DNA templates can be conducted manually or through a computer system. In a preferred embodiment, the methods according to the present invention are conducted through the use of
5 a computer system.

A computer system according to the present invention refers to a computer or a computer readable medium designed and configured to perform some or all of the methods as described herein. A computer used herein may be any of a variety of types of general-purpose computers such as a personal computer, network server, workstation, or other computer
10 platform now or later developed. As commonly known in the art, a computer typically contains some or all the following components, for example, a processor, an operating system, a computer memory, an input device, and an output device. A computer may further contain other components such as a cache memory, a data backup unit, and many other devices. It will be understood by those skilled in the relevant art that there are many possible
15 configurations of the components of a computer.

A processor used herein may include one or more microprocessor(s), field programmable logic arrays(s), or one or more application specific integrated circuit(s). Illustrative processors include, but are not limited to, Intel Corp.'s Pentium series processors, Sun Microsystems' SPARC processors, Motorola Corp.'s PowerPC processors, MIPS
20 Technologies Inc.'s MIPs processors, and Xilinx Inc.'s Vertex series of field programmable logic arrays, and other processors that are or will become available.

A operating system used herein comprises machine code that, once executed by a processor, coordinates and executes functions of other components in a computer and

facilitates a processor to execute the functions of various computer programs that may be written in a variety of programming languages. In addition to managing data flow among other components in a computer, an operating system also provides scheduling, input-output control, file and data management, memory management, and communication control and related services, all in accordance with known techniques. Exemplary operating systems include, for example, a Windows operating system from the Microsoft Corporation, a Unix or Linux-type operating system available from many vendors, any other known or future operating systems, and some combination thereof.

A computer memory used herein may be any of a variety of known or future memory storage devices. Examples include any commonly available random access memory (RAM), magnetic medium such as a resident hard disk or tape, an optical medium such as a read and write compact disc, or other memory storage devices. A memory storage device may be any of a variety of known or future devices, including a compact disk drive, a tape drive, a removable hard disk drive, or a diskette drive. Such types of memory storage device typically read from, and/or write to, a computer program storage medium such as, respectively, a compact disk, magnetic tape, removable hard disk, or floppy diskette. Any of these computer program storage media, or others now in use or that may later be developed, may be considered a computer program product. As will be appreciated, these computer program products typically store a computer software program and/or data. Computer software programs, also called computer control logic, typically are stored in system memory and/or the program storage device used in conjunction with memory storage device.

In one embodiment, a computer program product as described herein comprising a computer memory having a computer software program stored therein, wherein the computer

software program when executed by a processor or in a computer performs methods according to the present invention.

An input device used herein may include any of a variety of known devices for accepting and processing information from a user, whether a human or a machine, whether local or remote. Such input devices include, for example, modem cards, network interface cards, sound cards, keyboards, or other types of controllers for any of a variety of known input function. An output device may include controllers for any of a variety of known devices for presenting information to a user, whether a human or a machine, whether local or remote. Such output devices include, for example, modem cards, network interface cards, sound cards, display devices (for example, monitors or printers), or other types of controllers for any of a variety of known output function. If a display device provides visual information, this information typically may be logically and/or physically organized as an array of picture elements, sometimes referred to as pixels.

As will be evident to those skilled in the relevant art, a computer software program of the present invention can be executed by being loaded into a system memory and/or a memory storage device through one of the above input devices. On the other hand, all or portions of the software program may also reside in a read-only memory or similar type of memory storage device, such devices not requiring that the software program first be loaded through input devices. It will be understood by those skilled in the relevant art that the software program or portions of it may be loaded by a processor in a known manner into a system memory or a cache memory or both, as advantageous for execution.

As will be appreciated by those skilled in the art, a computer program product of the present invention, or a computer software program of the present invention, may be stored on

and/or executed in a PCR instrument. For example, a computer software of the present invention can be installed in, for example, the Smart Cycler System, the Idaho Rapid Cycler, the Carbett Roter-Gene System, the GeneAmp 5700 Sequence Detection System, the ABI Prism7000, 7700 & 7900 Sequence Detection Systems, the iCycler System, the MX-4000
5 Multiplex Quantitative PCR System, the DNA Engine Opticon System, the Perkin-Elmer 9600 cycler, and MJ Research's DNA Engine Opticon System.

However, it is not necessary that the computer program product or the computer software program be stored on and/or executed in a PCR instrument. Rather, the computer product or software may be stored in a separate computer or a computer server which may or
10 may not connect to the PCR instrument through a data cable, a wireless connection, or a network system. As commonly known in the art, network systems comprise hardware and software to electronically communicate among computers or devices. Examples of network systems may include arrangement over any media including Internet, Ethernet 10/1000, IEEE 802.11x, IEEE 1394, xDSL, Bluetooth, 3G, or any other ANSI approved standard.

15 In a preferred embodiment, a computer program termed MULTIPLEX is developed to select primers according to the methods as described in the present invention. See Table I for the flowchart of MULTIPLEX program.

Even with the assistance of MULTIPLEX, it is time consuming to analyze exhaustively all possible sequences frames and select the best possible frames for PCR
20 primers. To expedite the computer-assisted selection process, a strategy termed "random fitting" is developed. Under the random fitting strategy, a set of criteria for the length of the matching sequences is set forth for primer selection. See Table I.. For example, when the number of 3' end matching bases is less than 4, the experimental effect of this

complementarity is neglected. Therefore, the criterion for the length of 3' end complementarity was set to be less than four. With the predefined criteria, the MULTIPLEX computer program first randomly picks up a pair of primers for each target sequence. All possible interacting pairs in this combination are examined. Record is made on qualified and unqualified primers in the combination. The program then randomly picks up a new pair of primers for each target sequence that collectively form a second combination. If the number of qualified primers in the second combination is less than that in the first combination, no record is made. The MULTIPLEX program, however, begins to examine a third combination. If the number of qualified primers in the third combination is greater than that in the first combination, the first primer combination is replaced by the third one in record. The program keeps processing until a combination with all qualified primers is found. Under the random fitting strategy, the MULTIPLEX program can select qualified primers for 100 sequences within two hours, 500 within two days and 1,000 within two weeks. The "qualified primers" are those primers fully conforming with the selection criteria set forth in the method of the present invention.

To further improve the MULTIPLEX program, another primer selection method called linear primer selection is also used as an alternative. See Table I. With this strategy, instead of selecting the frames randomly, each frame of a pair is selected from one end of the defined range of a sequence. The selected frame pair is then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding sequence is completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences. The newly selected frames are then examined. If these frames are qualified as primer sequences, the selection of primers for the corresponding

sequence is then completed. Otherwise, the selection will be continued by sliding the frames by one base toward the other ends of the sequences... If the frames are slid to the other ends but not qualified frames are found, the lengths of the frames will be increased by 1 base. The same process described above will be repeated. The sliding and length changing process repeats until a pair of qualified frames is found. If no qualified frames can be found after exhausting all possible frames for a sequence, the sequence will be labeled as unusable, and will be excluded from the multiplex set. This method is called linear primer selection.

When the number of sequences is large, the random primer selection method may be used for selecting primers of only a fraction of sequences. The random selection process is stopped at a point defined by the user. The program can then switch to linear primer selection method. We have shown that appropriate combination of these two methods can increase the selection speed by several tens to >100 fold compared with using the random method only.

It needs to be pointed out that the MULTIPLEX method can be used not only for primer selection of SNPs, but also for primer selection of any other DNA and RNA sequences if a position is defined so that it can be used to separate a sequence into two parts for selecting the two primers, respectively.

Following the selecting and synthesizing of qualified primers, DNA templates are contacted with multiple primers for the amplification of desired DNA fragments under conditions suitable for multiplex PCR developed in the inventor's laboratory. These conditions are: 2.0 mM MgCl₂, 50 mM KCl, 100 mM Tris-HCl, pH 8.3, 100 μM deoxynucleotide triphosphates (dNTPs), and 10 units/50 μl "HotStart" *Taq* DNA polymerase (Qiagen, Valencia CA). The PCR mix is first preheated for 15 min at 94°C to activate the DNA polymerase followed by 40 PCR cycles. Each cycle consists of a denaturation step at

94°C for 40 sec, and then an annealing step at 55°C for 2 min followed by a ramping step from 55°C to 70°C within 5 min. After the PCR cycles, the samples are incubated at 72°C for 3 min.

A DNA template to be used in practicing the present invention includes without
5 limitation eukaryotic, prokaryotic and viral DNA. The DNA may be obtained from any cell source or body fluid. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Body fluids include blood, urine, cerebrospinal fluid, semen and tissue exudates at the site of infection or inflammation. DNA
10 is extracted from the cell source or body fluid using any of the numerous methods that is standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source. The preferred amount of DNA to be extracted for use in the present invention is at least 5 pg which is corresponding to about 1 human cell equivalent of a genome size of 4×10^9 base pairs.

15 A primer designed in accordance to the method in the present invention is from 17 to 50 nucleotides in length, preferably 20 to 35 nucleotides in length. The concentration of a primer in the multiplex PCR reaction can range from 0.1nM to about 4μM per reaction, preferably from 1nM to 0.1 4μM per reaction.

Multiplex PCR reactions are carried out using manual or automatic thermal cycling.
20 Any commercially available thermal cycler may be used, such as, e.g., a Perkin-Elmer 9600 cycler.

The resultant multiple amplified DNA fragments of interest are analyzed using any of several methods that are well-known in the art. For example, agarose or polyacrylamide gel

electrophoresis is used to rapidly resolve and identify each of the amplified sequences. When a gel is used, different amplified sequences are preferably of distinct sizes and thus can be resolved in a single gel. The reaction mixture can further be treated with one or more restriction endonucleases prior to electrophoresis. Alternative methods of product analysis include without limitation dot-blot hybridization with allele-specific oligonucleotides, single-strand conformational polymorphism analysis, high-throughput genotyping platforms including oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization, molecular beacon genotyping, DNA chip-based microarray, and mass spectrometry technology.

The multiple primers designed in accordance to the method in the present invention minimize the nonspecific interaction between primers or between a primer and nonspecific target sequence of a template DNA. Accordingly, the use of these primers in a multiplex PCR minimizes the formation of non-specific extension of undesired DNA fragments and maximizes the specific interaction and amplification of desired DNA fragments.

Furthermore, the method in the present invention increases the number of desired DNA fragments, enhances the efficacy of the multiplex PCR and achieves a significant reduction in cost, time and sample volume. Finally, the multiple primers designed in accordance with the methods of the present invention may be used in real time PCR or multiplex real time PCR.

A single multiplex PCR using primers designed by the present invention can contain at least 50 pairs of primers and produce at least 50 desired DNA fragments. It is preferred that the single multiplex PCR contain at least 100 pairs of primers and produce at least 100 desired DNA fragments.

The present invention significantly broadens the application of multiplex PCR in the art which has been limited by the nonspecific extensions of unwanted DNA fragment and the number of desired DNA fragments it could produce. Given a large number of multiple desired DNA fragments that a multiplex PCR now can produce using primers designed under the present invention, the multiplex PCR can now be fully used in applications including but not limited to the identification of multiple genes related to multifactorial diseases, the genome-scale detection of genetic alterations in cancers, the studies in large-scale pharmacogenetic reactions, the genotyping genetic polymorphism in a large population, and the gene expression profiling in various samples.

The following examples are intended to further illustrate the present invention without limiting the invention thereof.

EXAMPLE 1. Selection of 627 pairs of primers.

648 single nucleotide polymorphism (SNP) markers were initially selected from the SNP Database maintained by the National Center for Biotechnology Information. To facilitate the genotyping after PCR, all these SNPs were transition polymorphisms that were A to G or C to T changes at their polymorphic sites. All SNP sequences were analyzed by the computer program MULTIPLEX to determine whether these SNP sequences are unique in the genome. The repetitive sequences were discarded. PCR primers were selected by using the computer program MULTIPLEX described above with the following values: T_m range = 75-104°C, primer length range = 24-33 bases, 3' perfect matches <4, 3' match with 1 mismatch <7, 3' end matching internal sequences of other molecules <9; 3' end matches internal sequences of other molecules with 1 mismatch <11; maximal match between different molecules, 75%). The quality of each pair of primers was examined individually by using them to amplify their

target sequences. Only the primer pairs with high specificity and yield, as judged by gel electrophoresis, were used for multiplex amplification. At the end, a panel of 627 SNPs was selected from the initial 648 SNPs as shown in Table II and Table III. Table II is an illustration of a list of 627 single nucleotide polymorphism (SNP) markers selected from 648 SNP markers. Table 3 is an illustration of a list of 627 pairs of primers and probes that were designed according to the method disclosed in the embodiment of the invention, used in a single multiplex PCR reaction, and used for genotype determination by analyzing the multiplex PCR products by microarray.

EXAMPLE 2. Using 622 pairs of selected primers in a single multiplex PCR.

For the multiplex PCR, lysate for 500 cells from a tissue cultured cell line, MG2314, was prepared. The reason for using cells instead of purified DNA is that they could be precisely quantified and equal number of nearly equal number of copies of the target sequences could be used as the starting material. PCR mix contained 1 X PCR buffer (100 mM Tris-HCl pH 8.3, 150 mM KCl, 1.5 mM MgCl₂, and Gelatin 100 µg/ml), primers (10 nM each) for all SNPs, the four dNTPs (100 µM each), Taq DNA polymerase (5 units) with a final volume of 30 µl. Sample was preheated for 15 min at 95°C. Each PCR cycle consisted of a denaturation step at 95°C for 40 sec; annealing at 55°C for 3 min; and a step for both annealing and extension with temperature ramping from 55°C to 70°C within 5 min. A 3 min incubation at 95 °C as added after the PCR cycle to minimize the incompletely extended PCR products. PCR was completed after 40 cycles.

EXAMPLE 3. Analysis of multiple DNA fragments after the multiplex PCR

To resolve the allelic products in the multiplex PCR product for genotype determination, single base extension and microarray methods were used. Two

oligonucleotides with completely complementary sequences for each SNP were synthesized for this purpose. One of these was called E probe that was using in the single base extension assay. The other was called A probe that was spotted onto a coated glass slide. E probes had sequences with their 3'-ends next to their polymorphic sites. In the single base extension
5 assay, dideoxynucleotides labeled with either the chromophore Cy 3 or Cy 5 were used. The allelic base at the polymorphic site determined which fluorescently labeled nucleotide could be incorporated into an E probe.

The corresponding A probes were spotted onto a glass slide with a microarrayer manufactured by Cartesian. The fluorescently labeled E probes were hybridized with the A
10 probes on the microarray. The signal intensity for the alleles of each SNP was determined by using the computer software for image analysis from Biodiscovery. See, Fig. 3.

To validate the results from microarray analysis, the genotypes of the cell line used in the study were determined for all 622 SNPs by restriction enzyme digestion method described by Li & Hood, Multiplex Genotype Determination at A DNA Sequence Polymorphism
15 Cluster in The Human Immunoglobulin Heavy-Chain Region, *Genomics* 26: 199-206 (1995). A few SNPs that could not be analyzed by this method were analyzed by direct sequence analysis.

Because all SNP were transition polymorphisms, all E probes could be analyzed by either A and G or T and C. In either case, consistent results from 85% (for labeling with A
20 and G) to 90% (for labeling with T and C) SNPs were obtained by both microarray and the restriction digestion methods. A probes for A and G labeling were used for 85% of SNPs, and others were replaced by those for T and C labeling. Fig. 5.

Papers and patents listed in the disclosure are expressly incorporated by reference in their entirety. It is to be understood that the description, specific examples, and figures, while indicating preferred embodiments, are given by way of illustration and exemplification and are not intended to limit the scope of the present invention. Various changes and

5 modifications within the present invention will become apparent to the skilled artisan from the disclosure contained herein. Therefore, the spirit and scope of the appended claims should not be limited to the description of the preferred versions contained herein.

Flow Chart - General

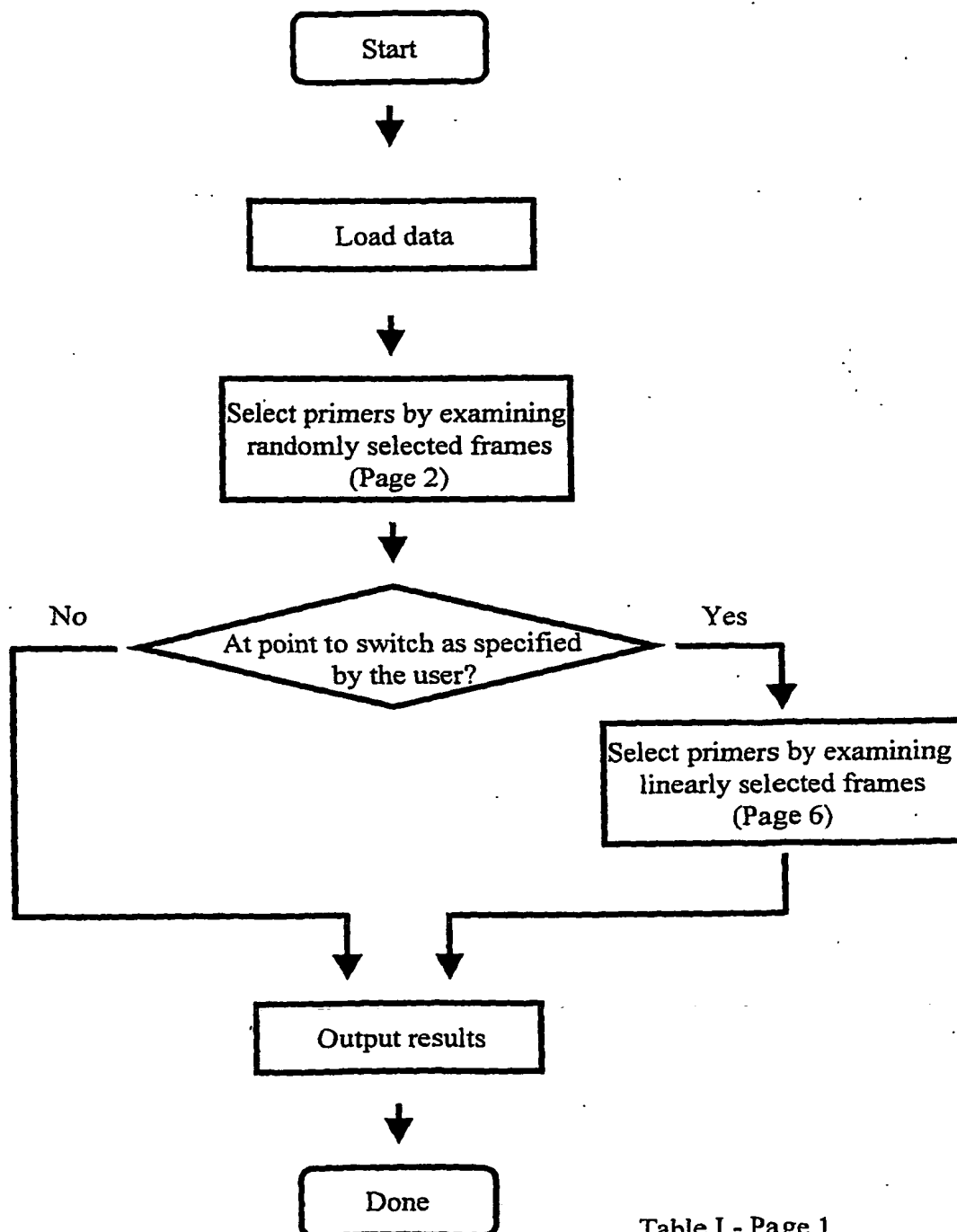


Table I - Page 1

Page 2 – Select Primers by Examining Randomly Selected Frames

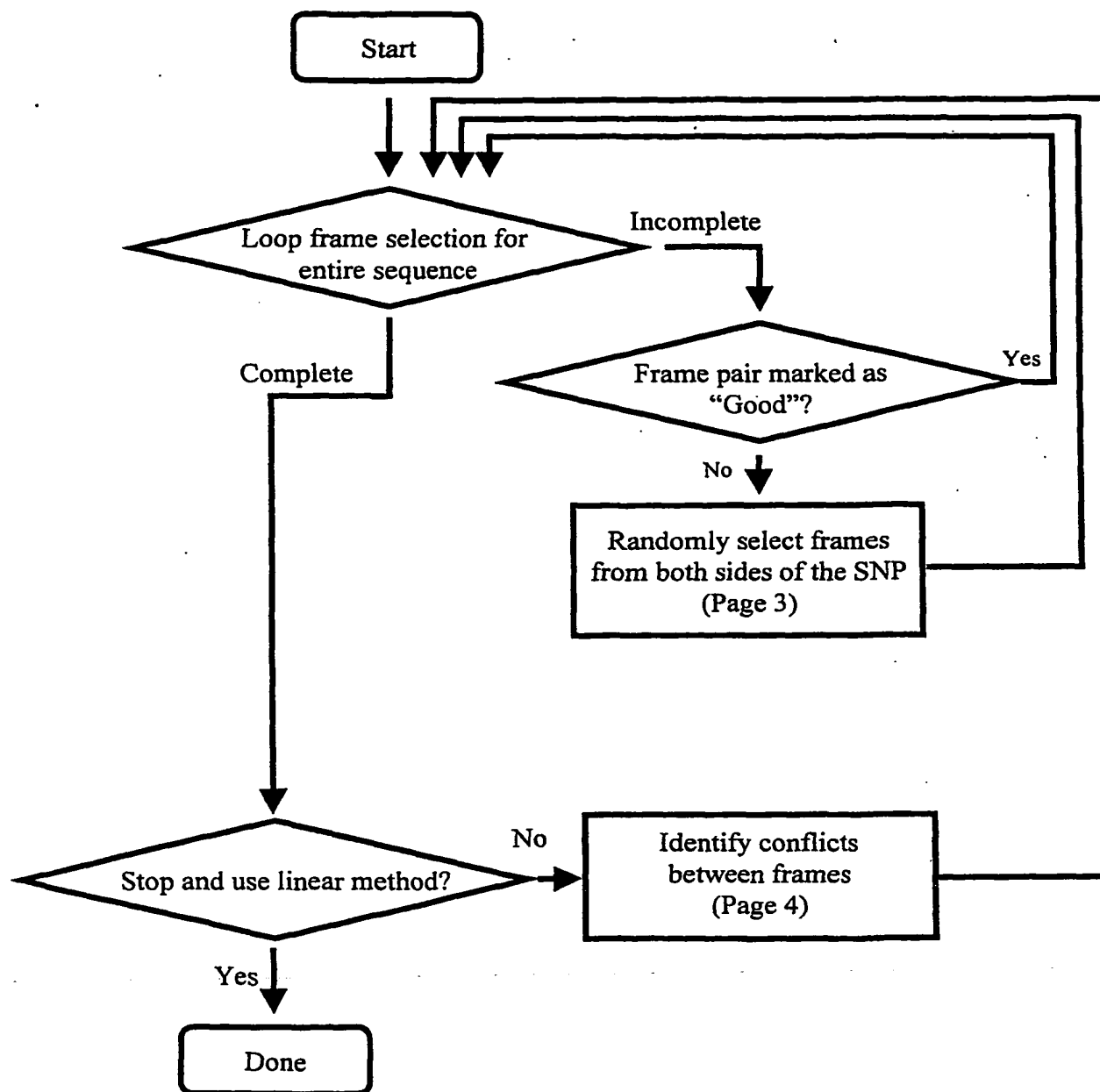


Table I - Page 2

Page 3 - Randomly Select Frames from Both Sides of Each SNP

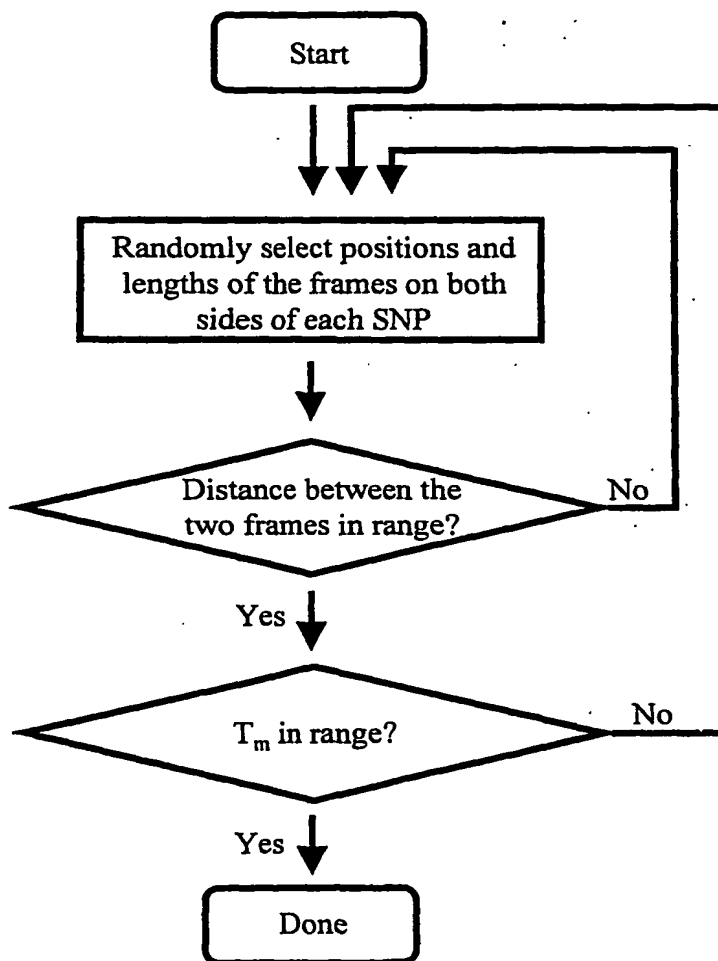


Table I - Page 3

Page 4 - Identify Conflicts between Frames

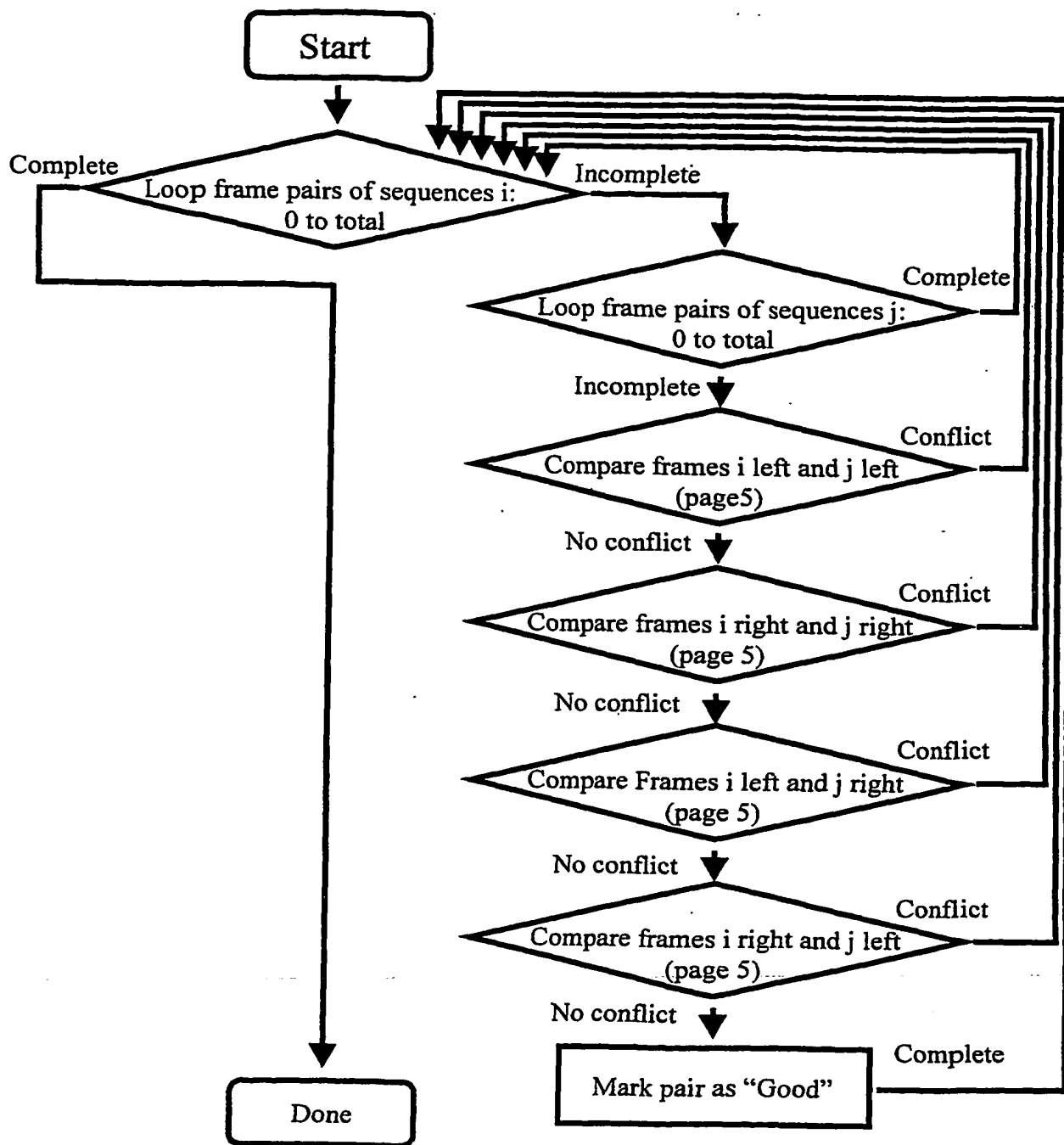


Table I - Page 4

Page 5 – Compare Selected Frames

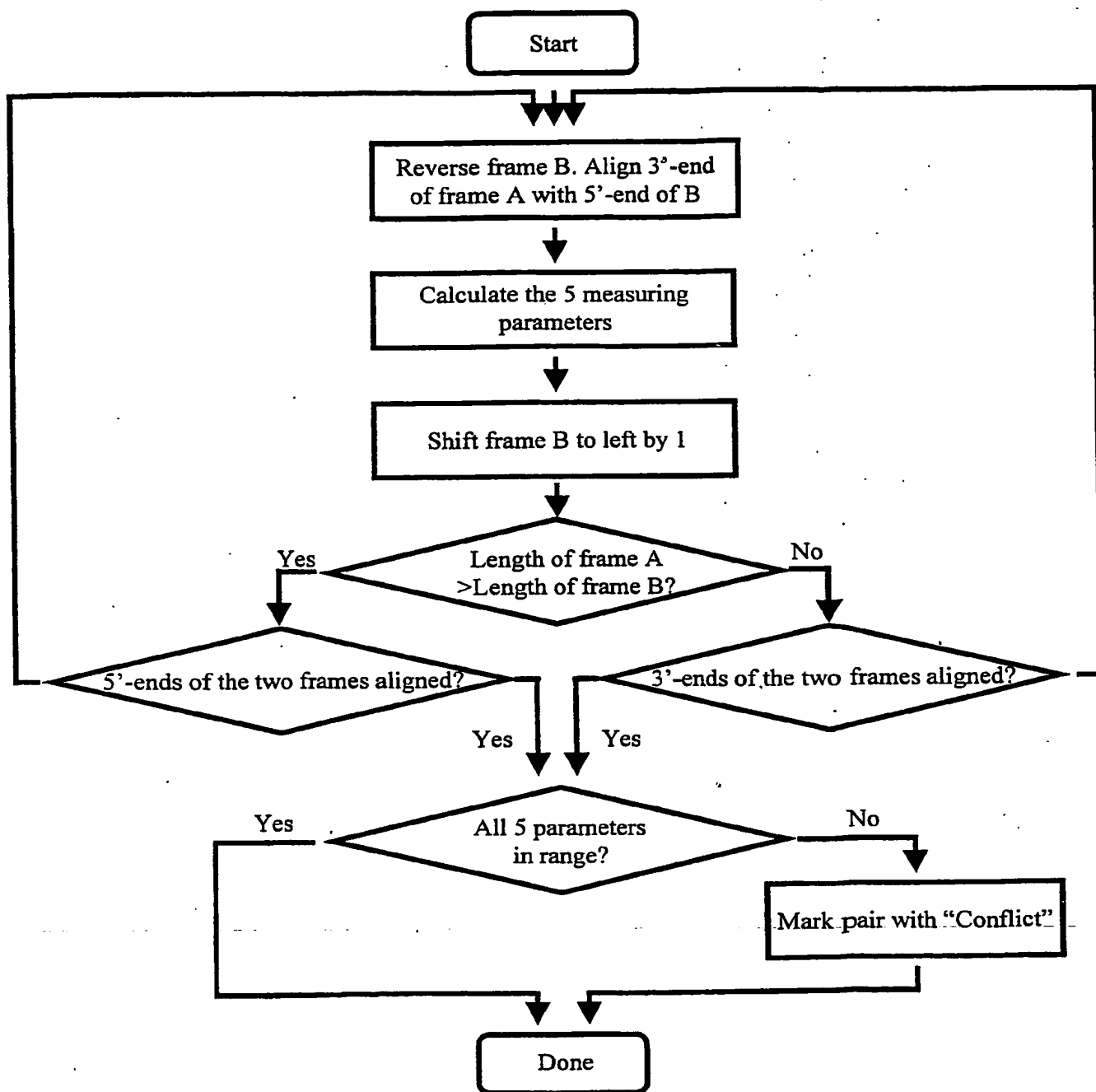


Table I - Page 5

Page 6 - Select Primers by Examining Linearly Selected Frames

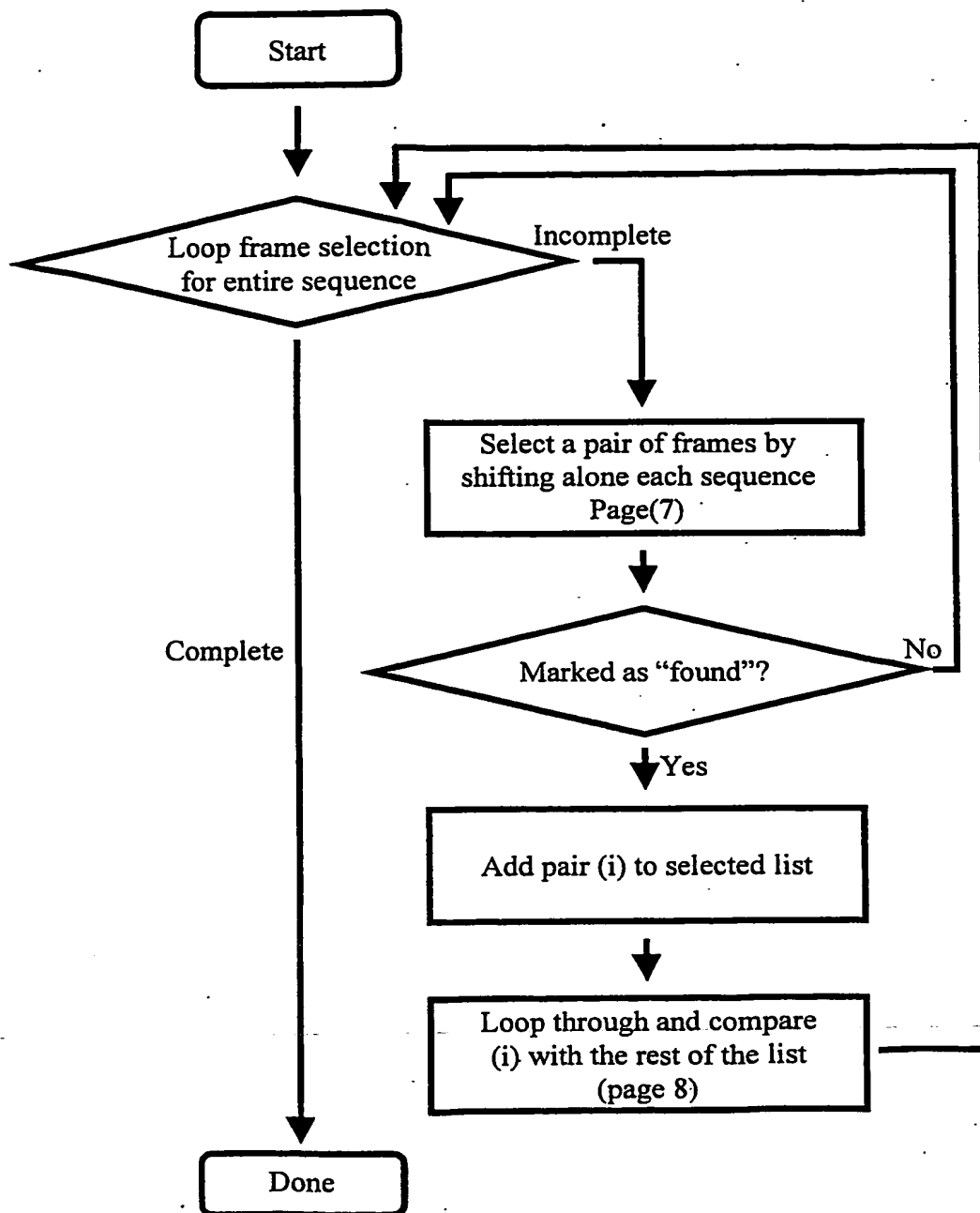


Table I - Page 6

Page 7 – Select a pair of frames by shifting alone each sequence

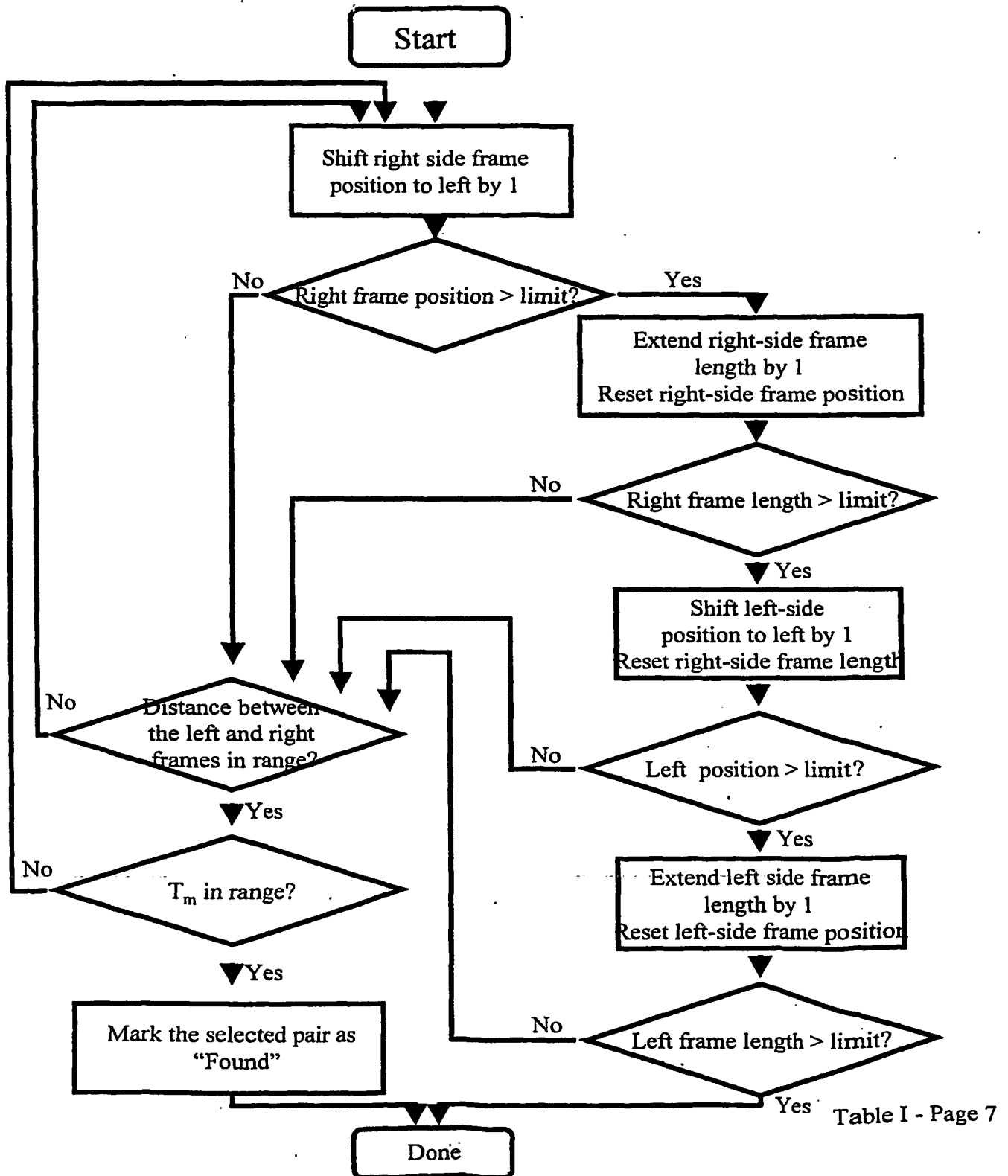


Table I - Page 7

Page 8 - Loop through and Compare Frames i with the Rest of the List

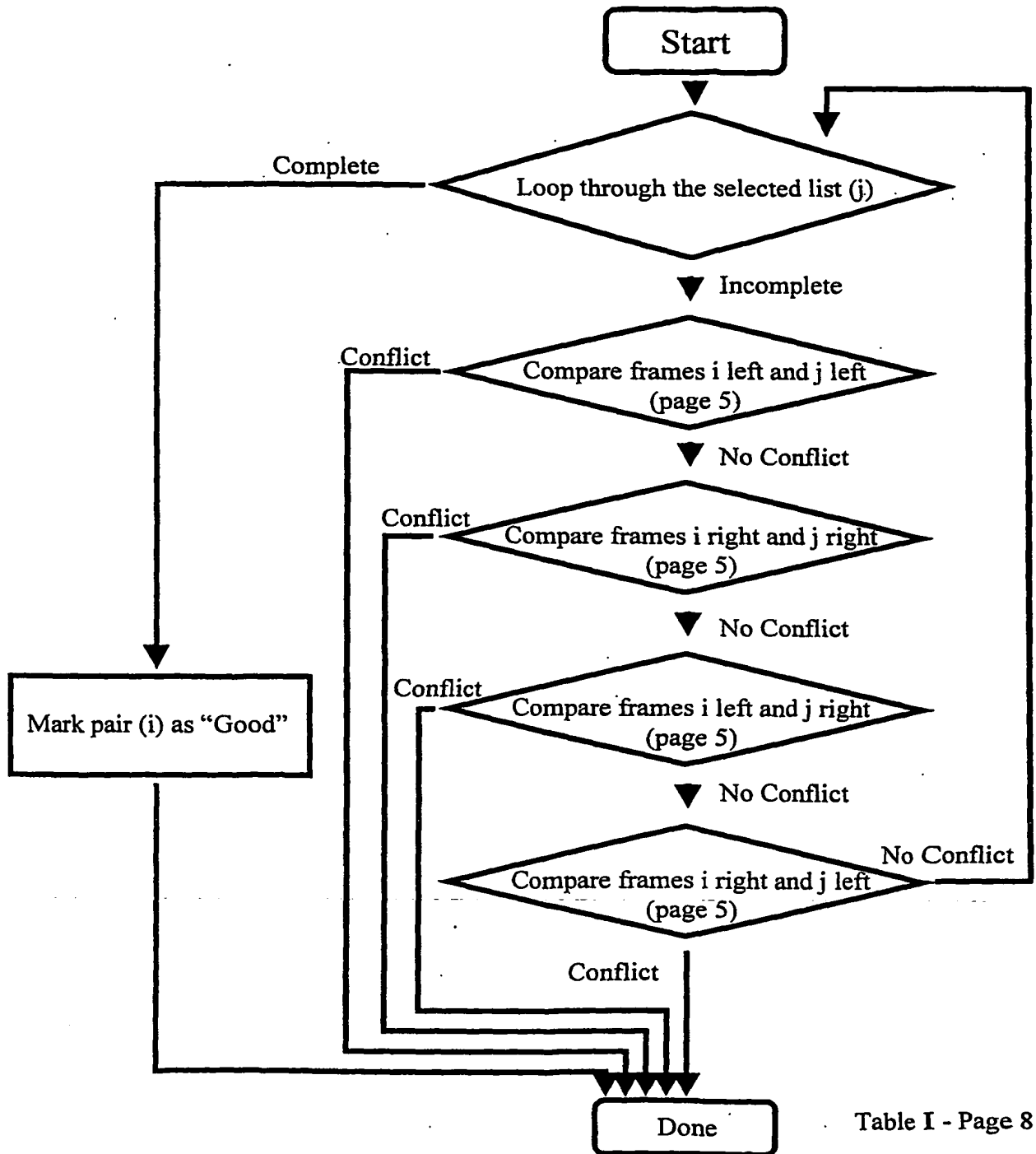


Table I - Page 8

Table 2 Oligonucleotides Used as PCR Primers and as Probes for Genotyping

SNP	Left Primer		Right Primer		Tabled Probe		Probe on Slide	
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
01T002L	01T002L	CACGTGTGAGGCTTTGGTCC	01T002R	GCTCTACCTCTGGACACTCGGGGG	01T002E	GCTCCCACTGCTTCCCGGCAATC	01T002A	GAATGCGGGAAGGAGGAGG
01T003L	01T003L	CTATAGCCCTCTGAATGGTC	01T003R	TTCTGCTTCCCGGAGGAGC	01T003E	GCTGAAAGCAATAATAGATGTCAGAC	01T003A	GTCGTGACACCAATATGCTTTCAGC
01T004L	01T004L	AAAGAAGAGAGGTTTGGGGAT	01T004R	CACATGCTGACAGCCGAGAGACTC	01T004E	CTTTCATTACAGCTAGAAATATAGATGTC	01T004A	GCAATCTAAATTTCTAGCTGTAAATAAG
01T005L	01T005L	ACTAAGGAGGATCAACAACCTC	01T005R	AAGCACTCTTCTTACGTCC	01T005E	CTTGTGTGGGCTGTGTGTGACACC	01T005A	GGCTGACACGAGCCCAACCAAGTC
01T006L	01T006L	GTACGGTGTCTACAGCAACCA	01T006R	GGAAGCAGCTGTGAGTGGGGGG	01T006E	GATGATTTCTTCCGACCTTATCTATCTC	01T006A	TTTAGCCCAAGCCCAAGCCAGCAG
01T007L	01T007L	CAACTGAGAGTGTAGTATTTGGA	01T007R	TAGCATCCCAAGCTCTCTTGA	01T007E	GATGATTTCTTCCGACCTTATCTATCTC	01T007A	GAGATTAAATAGGTGAGCAAAATTAATC
01T008L	01T008L	GAATTTCTATCTCACACCGCTGA	01T008R	AGGCTGCTCTCTCTTCAAC	01T008E	GCTTTATCAAGAGGGGTATAAAGGT	01T008A	ATCTTTATACCCCTGCTGTATTAAGC
01T009L	01T009L	ACAGCTGTCTACAGAGGTC	01T009R	TTCTCTCTCTGGATGCTTATG	01T009E	GGCAGAGATGAGTCTCAGGACTTGTAA	01T009A	TTCAACAAGTCTCTAACAATCTCTGTC
01T010L	01T010L	CTAGGCCCACTCTGAGAGGCTA	01T010R	GTCTCTCTCTCTGAGGCTCC	01T010E	GGCCCAATTTCTTATTCACCTTTGCT	01T010A	AGCAAAAGTGAATAGAAATATGAGGC
01T011L	01T011L	AACACTTCTGCTGATATAGTAG	01T011R	GAATGGATGAGACACTCAAT	01T011E	GCTTAAGAAGCCAGACAGACTCTCTG	01T011A	CAGGAATGCTGCTGCTTCTTACGC
01T012L	01T012L	AGATTTCTTGGACCTCTCTT	01T012R	AAAAGATAGATTAACAGGTGAC	01T012E	TTTGCCAGTGCATCAAGAGGAC	01T012A	GTCCTCTCTGATGCTGCTGACCA
01T013L	01T013L	AAGGCAATAACTGACTGCTGA	01T013R	GTACATGCTGCTGCTCAACGC	01T013E	GATTTTCAAGGTAGGCGAGGAAAG	01T013A	TTTCTCTGCTGCTGCTTGAATTC
01T014L	01T014L	CCAGCGGAGAGCTGTGAAATAG	01T014R	GAAAGCAGCTGCGGTCTGCTCC	01T014E	AGGCAAGGAGGAGAGGGGAGGTT	01T014A	AACCTCTCTCTGCTGCTGCTGCT
01T015L	01T015L	AAATTAGGCTTTATGTAATTCAG	01T015R	TATGAGGCTGCTTAAATTC	01T015E	GGGTCAAGAGCTGACTCTGCTCACTTA	01T015A	TAAGTGGAGAGTCAAGGCTTGAACCC
01T016L	01T016L	CAAAAGCTCTCAAGTCTTAAAAA	01T016R	TATGAGGCTGCTTAAATTC	01T016E	GGGTCAAGAGCTGACTCTGCTCACTTA	01T016A	AGGTATTCGGCAAGATCTCTTAAAC
01T017L	01T017L	GTGCTCATGAGCCGACAGGGG	01T017R	AGGCTGCTGAGCAGGGGAC	01T017E	GCTGAGAGAGGCTCTGCTGCTGCTG	01T017A	CGGCCACCGGGGCGCTGCTCAGC
01T018L	01T018L	CTATAGGCTCTCAAGTCTTAACTAA	01T018R	CCCTGAGCTGCTGCTGCTGCTG	01T018E	CTGCGCTGCTGCTGCTGCTGCTG	01T018A	CTTCCAGAACTAGTACAGGGCCAG
01T019L	01T019L	CTTACGAGGCGGACAGCC	01T019R	TCAAGGCTCTCTTAAAGGACTC	01T019E	CACCATGCTCTACAGCAACTCAACCC	01T019A	GGGTAGGCTTGTATAGCCATGCTG
01T020L	01T020L	CTCTCTAGTAAACCCGACCT	01T020R	GGCTCTCTAGAGCTCTCAAT	01T020E	GATCATCATCATTAACATAGGGCAT	01T020A	ATGCCCTATTTTATGATGATGATCTC
01T021L	01T021L	CTCTAGTGTGCTGGGCTG	01T021R	GGGCAAGTGAAGCTGAGGAGTGG	01T021E	GGCCCTGCTGCTTCCACAGGCTGCT	01T021A	AGCCAGGCTAGGAACAGGGGCTC
01T022L	01T022L	CTACTCCCTAGGCTCCGC	01T022R	AGGCAAGTGAAGCTGAGGAGTGG	01T022E	GGCCCTGCTGCTTCCACAGGCTGCT	01T022A	AGCCAGGCTAGGAACAGGGGCTC
01T023L	01T023L	ATTCGAACTTTACAGCAC	01T023R	AGGCAAGTGAAGCTGAGGAGTGG	01T023E	GGCCCTGCTGCTTCCACAGGCTGCT	01T023A	AGCCAGGCTAGGAACAGGGGCTC
01T024L	01T024L	CTGAAACACCGGTTATAG	01T024R	AGGCAAGTGAAGCTGAGGAGTGG	01T024E	GGCCCTGCTGCTTCCACAGGCTGCT	01T024A	AGCCAGGCTAGGAACAGGGGCTC
01T025L	01T025L	CTGAAACACCGGTTATAG	01T025R	AGGCAAGTGAAGCTGAGGAGTGG	01T025E	GGCCCTGCTGCTTCCACAGGCTGCT	01T025A	AGCCAGGCTAGGAACAGGGGCTC
01T026L	01T026L	CTGAAACACCGGTTATAG	01T026R	AGGCAAGTGAAGCTGAGGAGTGG	01T026E	GGCCCTGCTGCTTCCACAGGCTGCT	01T026A	AGCCAGGCTAGGAACAGGGGCTC
01T027L	01T027L	CTGAAACACCGGTTATAG	01T027R	AGGCAAGTGAAGCTGAGGAGTGG	01T027E	GGCCCTGCTGCTTCCACAGGCTGCT	01T027A	AGCCAGGCTAGGAACAGGGGCTC
01T028L	01T028L	CTGAAACACCGGTTATAG	01T028R	AGGCAAGTGAAGCTGAGGAGTGG	01T028E	GGCCCTGCTGCTTCCACAGGCTGCT	01T028A	AGCCAGGCTAGGAACAGGGGCTC
01T029L	01T029L	CTGAAACACCGGTTATAG	01T029R	AGGCAAGTGAAGCTGAGGAGTGG	01T029E	GGCCCTGCTGCTTCCACAGGCTGCT	01T029A	AGCCAGGCTAGGAACAGGGGCTC
01T030L	01T030L	CTGAAACACCGGTTATAG	01T030R	AGGCAAGTGAAGCTGAGGAGTGG	01T030E	GGCCCTGCTGCTTCCACAGGCTGCT	01T030A	AGCCAGGCTAGGAACAGGGGCTC
01T031L	01T031L	CTGAAACACCGGTTATAG	01T031R	AGGCAAGTGAAGCTGAGGAGTGG	01T031E	GGCCCTGCTGCTTCCACAGGCTGCT	01T031A	AGCCAGGCTAGGAACAGGGGCTC
01T032L	01T032L	CTGAAACACCGGTTATAG	01T032R	AGGCAAGTGAAGCTGAGGAGTGG	01T032E	GGCCCTGCTGCTTCCACAGGCTGCT	01T032A	AGCCAGGCTAGGAACAGGGGCTC
01T033L	01T033L	CTGAAACACCGGTTATAG	01T033R	AGGCAAGTGAAGCTGAGGAGTGG	01T033E	GGCCCTGCTGCTTCCACAGGCTGCT	01T033A	AGCCAGGCTAGGAACAGGGGCTC
01T034L	01T034L	CTGAAACACCGGTTATAG	01T034R	AGGCAAGTGAAGCTGAGGAGTGG	01T034E	GGCCCTGCTGCTTCCACAGGCTGCT	01T034A	AGCCAGGCTAGGAACAGGGGCTC
01T035L	01T035L	CTGAAACACCGGTTATAG	01T035R	AGGCAAGTGAAGCTGAGGAGTGG	01T035E	GGCCCTGCTGCTTCCACAGGCTGCT	01T035A	AGCCAGGCTAGGAACAGGGGCTC
01T036L	01T036L	CTGAAACACCGGTTATAG	01T036R	AGGCAAGTGAAGCTGAGGAGTGG	01T036E	GGCCCTGCTGCTTCCACAGGCTGCT	01T036A	AGCCAGGCTAGGAACAGGGGCTC
01T037L	01T037L	CTGAAACACCGGTTATAG	01T037R	AGGCAAGTGAAGCTGAGGAGTGG	01T037E	GGCCCTGCTGCTTCCACAGGCTGCT	01T037A	AGCCAGGCTAGGAACAGGGGCTC
01T038L	01T038L	CTGAAACACCGGTTATAG	01T038R	AGGCAAGTGAAGCTGAGGAGTGG	01T038E	GGCCCTGCTGCTTCCACAGGCTGCT	01T038A	AGCCAGGCTAGGAACAGGGGCTC
01T039L	01T039L	CTGAAACACCGGTTATAG	01T039R	AGGCAAGTGAAGCTGAGGAGTGG	01T039E	GGCCCTGCTGCTTCCACAGGCTGCT	01T039A	AGCCAGGCTAGGAACAGGGGCTC
01T040L	01T040L	CTGAAACACCGGTTATAG	01T040R	AGGCAAGTGAAGCTGAGGAGTGG	01T040E	GGCCCTGCTGCTTCCACAGGCTGCT	01T040A	AGCCAGGCTAGGAACAGGGGCTC
01T041L	01T041L	CTGAAACACCGGTTATAG	01T041R	AGGCAAGTGAAGCTGAGGAGTGG	01T041E	GGCCCTGCTGCTTCCACAGGCTGCT	01T041A	AGCCAGGCTAGGAACAGGGGCTC
01T042L	01T042L	CTGAAACACCGGTTATAG	01T042R	AGGCAAGTGAAGCTGAGGAGTGG	01T042E	GGCCCTGCTGCTTCCACAGGCTGCT	01T042A	AGCCAGGCTAGGAACAGGGGCTC
01T043L	01T043L	CTGAAACACCGGTTATAG	01T043R	AGGCAAGTGAAGCTGAGGAGTGG	01T043E	GGCCCTGCTGCTTCCACAGGCTGCT	01T043A	AGCCAGGCTAGGAACAGGGGCTC
01T044L	01T044L	CTGAAACACCGGTTATAG	01T044R	AGGCAAGTGAAGCTGAGGAGTGG	01T044E	GGCCCTGCTGCTTCCACAGGCTGCT	01T044A	AGCCAGGCTAGGAACAGGGGCTC
01T045L	01T045L	CTGAAACACCGGTTATAG	01T045R	AGGCAAGTGAAGCTGAGGAGTGG	01T045E	GGCCCTGCTGCTTCCACAGGCTGCT	01T045A	AGCCAGGCTAGGAACAGGGGCTC
01T046L	01T046L	CTGAAACACCGGTTATAG	01T046R	AGGCAAGTGAAGCTGAGGAGTGG	01T046E	GGCCCTGCTGCTTCCACAGGCTGCT	01T046A	AGCCAGGCTAGGAACAGGGGCTC
01T047L	01T047L	CTGAAACACCGGTTATAG	01T047R	AGGCAAGTGAAGCTGAGGAGTGG	01T047E	GGCCCTGCTGCTTCCACAGGCTGCT	01T047A	AGCCAGGCTAGGAACAGGGGCTC
01T048L	01T048L	CTGAAACACCGGTTATAG	01T048R	AGGCAAGTGAAGCTGAGGAGTGG	01T048E	GGCCCTGCTGCTTCCACAGGCTGCT	01T048A	AGCCAGGCTAGGAACAGGGGCTC
01T049L	01T049L	CTGAAACACCGGTTATAG	01T049R	AGGCAAGTGAAGCTGAGGAGTGG	01T049E	GGCCCTGCTGCTTCCACAGGCTGCT	01T049A	AGCCAGGCTAGGAACAGGGGCTC
01T050L	01T050L	CTGAAACACCGGTTATAG	01T050R	AGGCAAGTGAAGCTGAGGAGTGG	01T050E	GGCCCTGCTGCTTCCACAGGCTGCT	01T050A	AGCCAGGCTAGGAACAGGGGCTC
01T051L	01T051L	CTGAAACACCGGTTATAG	01T051R	AGGCAAGTGAAGCTGAGGAGTGG	01T051E	GGCCCTGCTGCTTCCACAGGCTGCT	01T051A	AGCCAGGCTAGGAACAGGGGCTC
01T052L	01T052L	CTGAAACACCGGTTATAG	01T052R	AGGCAAGTGAAGCTGAGGAGTGG	01T052E	GGCCCTGCTGCTTCCACAGGCTGCT	01T052A	AGCCAGGCTAGGAACAGGGGCTC
01T053L	01T053L	CTGAAACACCGGTTATAG	01T053R	AGGCAAGTGAAGCTGAGGAGTGG	01T053E	GGCCCTGCTGCTTCCACAGGCTGCT	01T053A	AGCCAGGCTAGGAACAGGGGCTC
01T054L	01T054L	CTGAAACACCGGTTATAG	01T054R	AGGCAAGTGAAGCTGAGGAGTGG	01T054E	GGCCCTGCTGCTTCCACAGGCTGCT	01T054A	AGCCAGGCTAGGAACAGGGGCTC
01T055L	01T055L	CTGAAACACCGGTTATAG	01T055R	AGGCAAGTGAAGCTGAGGAGTGG	01T055E	GGCCCTGCTGCTTCCACAGGCTGCT	01T055A	AGCCAGGCTAGGAACAGGGGCTC
01T056L	01T056L	CTGAAACACCGGTTATAG	01T056R	AGGCAAGTGAAGCTGAGGAGTGG	01T056E	GGCCCTGCTGCTTCCACAGGCTGCT	01T056A	AGCCAGGCTAGGAACAGGGGCTC
01T057L	01T057L	CTGAAACACCGGTTATAG	01T057R	AGGCAAGTGAAGCTGAGGAGTGG	01T057E	GGCCCTGCTGCTTCCACAGGCTGCT	01T057A	AGCCAGGCTAGGAACAGGGGCTC
01T058L	01T058L	CTGAAACACCGGTTATAG	01T058R	AGGCAAGTGAAGCTGAGGAGTGG	01T058E	GGCCCTGCTGCTTCCACAGGCTGCT	01T058A	AGCCAGGCTAGGAACAGGGGCTC
01T059L	01T059L	CTGAAACACCGGTTATAG	01T059R	AGGCAAGTGAAGCTGAGGAGTGG	01T059E	GGCCCTGCTGCTTCCACAGGCTGCT	01T059A	AGCCAGGCTAGGAACAGGGGCTC
01T060L	01T060L	CTGAAACACCGGTTATAG	01T060R	AGGCAAGTGAAGCTGAGGAGTGG	01T060E	GGCCCTGCTGCTTCCACAGGCTGCT	01T060A	AGCCAGGCTAGGAACAGGGGCTC
01T061L	01T061L	CTGAAACACCGGTTATAG	01T061R	AGGCAAGTGAAGCTGAGGAGTGG	01T061E	GGCCCTGCTGCTTCCACAGGCTGCT	01T061A	AGCCAGGCTAGGAACAGGGGCTC
01T062L	01T062L	CTGAAACACCGGTTATAG	01T062R	AGGCAAGTGAAGCTGAGGAGTGG	01T062E	GGCCCTGCTGCTTCCACAGGCTGCT	01T062A	AGCCAGGCTAGGAACAGGGGCTC
01T063L	01T063L	CTGAAACACCGGTTATAG	01T063R	AGGCAAGTGAAGCTGAGGAGTGG	01T063E	GGCCCTGCTGCTTCCACAGGCTGCT	01T063A	AGCCAGGCTAGGAACAGGGGCTC
01T064L	01T064L	CTGAAACACCGGTTATAG	01T064R	AGGCAAGTGAAGCTGAGGAGTGG	01T064E	GGCCCTGCTGCTTCCACAGGCTGCT	01T064A	AGCCAGGCTAGGAACAGGGGCTC
01T065L	01T065L	CTGAAACACCGGTTATAG	01T065R	AGGCAAGTGAAGCTGAGGAGTGG	01T065E	GGCCCTGCTGCTTCCACAGGCTGCT	01T065A	AGCCAGGCTAGGAACAGGGGCTC
01T066L	01T066L	CTGAAACACCGGTTATAG	01T066R	AGGCAAGTGAAGCTGAGGAGTGG	01T066E	GGCCCTGCTGCTTCCACAGGCTGCT	01T066A	AGCCAGGCTAGGAACAGGGGCTC
01T067L	01T067L	CTGAAACACCGGTTATAG	01T067R	AGGCAAGTGAAGCTGAGGAGTGG	01T067E	GGCCCTGCTGCTTCCACAGGCTGCT	01T067A	AGCCAGGCTAGGAACAGGGGCTC
01T068L	01T068L	CTGAAACACCGGTTATAG	01T068R	AGGCAAGTGAAGCTGAGGAGTGG	01T068E	GGCCCTGCTGCTTCCACAGGCTGCT	01T068A	AGCCAGGCTAGGAACAGGGGCTC
01T069L	01T069L	CTGAAACACCGGTTATAG	01T069R	AGGCAAGTGAAGCTGAGGAGTGG	01T069E	GGCCCTGCTGCTTCCACAGGCTGCT	01T069A	AGCCAGGCTAGGAACAGGGGCTC
01T070L	01T070L	CTGAAACACCGGTTATAG	01T070R	AGGCAAGTGAAGCTGAGGAGTGG	01T070E	GGCCCTGCTGCTTCCACAGGCTGCT	01T070A	AGCCAGGCTAGGAACAGGGGCTC
01T071L	01T071L	CTGAAACACCGGTTATAG	01T071R	AGGCAAGTGAAGCTGAGGAGTGG	01T071E	GGCCCTGCTGCTTCCACAGGCTGCT	01T071A	AGCCAGGCTAGGAACAGGGGCTC
01T072L	01T072L	CTGAAACACCGGTTATAG	01T072R	AGGCAAGTGAAGCTGAGGAGTGG	01T072E	GGCCCTGCTGCTTCCACAGGCTGCT	01T072A	AGCCAGGCTAGGAACAGGGGCTC
01T073L	01T073L	CTGAAACACCGGTTATAG	01T073R	AGGCAAGTGAAGCTGAGGAGTGG	01T073E	GGCCCTGCTGCTTCCACAGGCTGCT	01T073A	AGCCAGGCTAGGAACAGGGGCTC
01T074L	01T074L	CTGAAACACCGGTTATAG	01T074R	AGGCAAGTGAAGCTGAGGAGTGG	01T074E	GGCCCTGCTGCTTCCACAGGCTGCT	01T074A	AGCCAGGCTAGGAACAGGGGCTC
01T075L	01T075L	CTGAAACACCGGTTATAG	01T075R	AGGCAAGTGAAGCTGAGGAGTGG	01T075E	GGCCCTGCTGCTTCCACAGGCTGCT	01T075A	AGCCAGGCTAGGAACAGGGGCTC
01T076L	01T076L	CTGAAACACCGGTTATAG	01T076R	AGGCAAGTGAAGCTGAGGAGTGG	01T076E	GGCCCTGCTGCTTCCACAGGCTGCT	01T076A	AGCCAGGCTAGGAACAGGGGCTC
01T077L	01T077L	CTGAAACACCGGTTATAG	01T077R	AGGCAAGTGAAGCTGAGGAGTGG	01T077E	GGCCCTGCTGCTTCCACAGGCTGCT	01T077A	AGCCAGGCTAGGAACAGGGGCTC
01T078L	01T078L	CTGAAACACCGGTTATAG	01T078R	AGGCAAGTGAAGCTGAGGAGTGG	01T078E	GGCCCTGCTGCTTCCACAGGCTGCT	01T078A	AGCCAGGCTAGGAACAGGGGCTC
01T079L	01T079L	CTGAAACACCGGTTATAG	01T079R	AGGCAAGTGAAGCTGAGGAGTGG	01T079E	GGCCCTGCTGCTTCCACAGGCTGCT	01T079A	AGCCAGGCTAGGAACAGGGGCTC
01T080L	01T080L	CTGAAACACCGGTTATAG	01T080R	AGGCAAGTGAAGCTGAGGAGTGG	01T080E	GGCCCTGCTGCTTCCACAGGCTGCT	01T080A	AGCCAGGCTAGGAACAGGGGCTC
01T081L	01T081L	CTGAAACACCGGTTATAG	01T081R	AGGCAAGTGAAGCTGAGGAGTGG	01T081E	GGCCCTGCTGCTTCCACAGGCTGCT	01T081A	AGCCAGGCTAGGAACAGGGGCTC
01T082L	01T082L	CTGAAACACCGGTTATAG	01T082R	AGGCAAGTGAAGCTGAGGAGTGG	01T082E	GGCCCTGCTGCTTCCACAGGCTGCT	01T082A	AGCCAGGCTAGGAACAGGGGCTC
01T083L	01T083L	CTGAAACACCGGTTATAG	01T083R	AGGCAAGTGAAGCTGAGGAGTGG	01T083E	GGCCCTGCTGCTTCCACAGGCTGCT	01T083A	AGCCAGGCTAGGAACAGGGGCTC
01T084L	01T084L	CTGAAACACCGGTTATAG	01T084R	AGGCAAGTGAAGCTGAGGAGTGG	01T084E	GGCCCTGCTGCTTCCACAGGCTGCT	01T084A	AGCCAGGCTAGGAACAGGGGCTC
01T085L	01T085L	CTGAAACACCGGTTATAG	01T085R	AGGCAAGTGAAGCTGAGGAGTGG	01T085E	GGCCCTGCTGCTTCCACAGGCTGCT	01T085A	AGCCAGGCTAGGAACAGGGGCTC
01T086L	01T086L	CTGAAACACCGGTTATAG	01T086R	AGGCAAGTGAAGCTGAGGAGTGG	01T086E	GGCCCTGCTGCTTCCACAGGCTGCT	01T086A	AGCCAGGCTAGGAACAGGGGCTC
01T087L	01T087L	CTGAAACACCGGTTATAG	01T087R	AGGCAAGTGAAGCTGAGGAGTGG	01T087E	GGCCCTGCTGCTTCCACAGGCTGCT	01T087A	AGCCAGGCTAGGAACAGGGGCTC
01T088L	01T088L	CTGAAACACCGGTTATAG	01T088R	AGGCAAGTGAAGCTGAGGAGTGG	01T088E	GGCCCTGCTGCTTCCACAGGCTGCT	01T088A	AGCCAGGCTAGGAACAGGGGCTC

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')
01T090L	01T090L	CAGCATGTTATAAAAGCTATATGGA	01T090R	GATCCACATGGTTCACTTAC	01T090E	CTTCTCTGACCACACAACTTAAATATGTA	01T090A	TTACAATTTTAAATTTGTTGTCAGGAAGG
01T091L	01T091L	ATTGGAGCCATATAAACAATATCTAA	01T091R	TATGTTGTTTAAATCTGCAAGTAT	01T091E	CATATAATTTTATCTCTCTGCCCACAA	01T091A	TTGTGGCCACAGAGTAAACAATATATG
01T094L	01T094L	TGGAAGTCCGCAAGTGA	01T094R	TACCTGTGCTATGACACAGATTTAT	01T094E	GCAACATGGCTATGAGAGCATCC	01T094A	GCATCTCCCTCCCTATGAGCTATGTC
01T096L	01T096L	TCAGTGCAGAAATGTTGGCTTA	01T096R	TGGTCCCTATGAGGATCTAGT	01T096E	CGACTCCCTTAATGTGGAGCTCAGACACT	01T096A	AGTGTCTGAGCTCCACATTAAGGAGTGC
01T097L	01T097L	CAGGCTGCTCTTCTGAGAGCGC	01T097R	AACTGATGAGGACAGATATAT	01T097E	GTCTGGTTCTTGTGGTGGCCG	01T097A	GTGGGTCAGTCCAGCCCTGAC
01T098L	01T098L	GGCCAGGTATAATACACTGGTAG	01T098R	ACTGAGGCCAGAGCGCATGAC	01T098E	GTCCGCTGGAAGTGGACCCCAA	01T098A	AGGCCAGGAGTATGATGTCAGGCA
01T099L	01T099L	CCATTGCTGTCTCCAGGCAAT	01T099R	TGTTAATTAATCTCCAGCCATCAG	01T099E	TGCTGCAATATACTACTCTCTGGCT	01T099A	AGGCCAGGAGTATGATGTCAGGCA
01T102L	01T102L	AGAGCCAGGTATCAAAAGTA	01T102R	CTCCCATCACTCTCTCAGCT	01T102E	CTTAGGCAACCGTGTGTGCTTTA	01T102A	TAAACAGCAGCCGCTGCTAGG
01T103L	01T103L	GACAGGTGATCAGACAGCTT	01T103R	ATCTGGCTCTCTCTGGAGTAT	01T103E	CTTCTATAAGAGGTGAGTATGATTAATGC	01T103A	GCATTAATTAATCACTCTCTCTTATAGAAC
01T104L	01T104L	CTGGAGAGCTCTCTCTCAAA	01T104R	ACATGATGACAGAAAGCTGTGA	01T104E	GAGCATGATTTTATAGTATTTATCTC	01T104A	GAGATAAATCACTCTCTCTTATAGAAC
01T105L	01T105L	AAATGTCTGCACTGCGCTC	01T105R	GAGGCCAGAGTACAGAAC	01T105E	CTCTGCTCCCTTATGATCCAAACAAAC	01T105A	GTCTGTTGGCATCAGGGGACAGAG
01T108L	01T108L	GGATGAGGAGGAAACAGCCGTGT	01T108R	TTCAATCTGCTGATCTCTGC	01T108E	GAAGTACATGCTGCAAGTCTTGAC	01T108A	AGAGGCTTTCTGACCATTTCAATTCAC
01T109L	01T109L	CATTGTGCTGTCTGCTCCCTC	01T109R	TGAATCGTATGAACCTTAC	01T109E	CAAGCTACATGCTGCAAGTCTTGAC	01T109A	GGTACACCACTTGAGCATGTAGCTG
01T111L	01T111L	GGCTATTGATGGAATAGTA	01T111R	ATACACATTTCTCATGTGTGTA	01T111E	GTGTGAGAGTAAATACATTTAAGATGG	01T111A	CCATCTTAAATGTTATTTACTCTCACAAC
01T117L	01T117L	GTCTCCATCTCTCTTAAAGGAAAA	01T117R	CTTTATTTTAAAGTCTCTTGACAG	01T117E	GCACATGATTTTAAATATAGCTTTTCC	01T117A	GGAAAGCTATTAATAAATAATCATGTC
01T118L	01T118L	TGCCAATCTCTCTGGCAAAATCAA	01T118R	TTATGATGGGAGTGTGTGTA	01T118E	AATGCTTCAAAACCCAGGGAAGCAG	01T118A	CTGCTCCCTGGGTTTGGAGCAT
01T119L	01T119L	GCAGAGGCTGATGGCAGTGAAC	01T119R	TCCCTTTTAAATCTCAACAT	01T119E	GCAGTGAACAAACAGATGATGATAGCTTAC	01T119A	GTAAAGCTATTAATCACTCTCTTTTCTCACTGC
01T120L	01T120L	CTATATCCCAATGCTTTGG	01T120R	TACAGGAGCTGCCACCACTCTG	01T120E	GGCAATATAGCAAGACCCCATTC	01T120A	GAATGGGCTCTGCTATATTTGCC
01T121L	01T121L	GAGGAGGTGAAGCAGATCA	01T121R	GGCAGTATTCGCCCTCTTA	01T121E	CTCAGGCTGCTGCTCTTTAGTGTG	01T121A	GACAAATAAAGACAGCCAGCTGAG
01T128L	01T128L	GGAGCTGCCAGAAACAGCTTG	01T128R	GTCCAGAGGAGGAGCGCTG	01T128E	CATGTGAGAGGACAGCTCTCCCATC	01T128A	GATGGAGGCTCTGCTCTCTCAGATG
01T129L	01T129L	ACCATAATGCCAGTTAATCTGAC	01T129R	GGGAGTCTGTGTCACACCTCAA	01T129E	CAAGCTCTTCCCACTCTAACTGTTC	01T129A	GACATGTTAAAGTGGGGGAAAGGTCTGG
01T131L	01T131L	CCCTGTTATTTTCCAGATAATCAG	01T131R	CTCTGATCTGACACAGCTAGGTA	01T131E	CAGTACAGTCTCTCAACACAGTAA	01T131A	TTACTGGTGTGATGAACAGCTGCTG
01T133L	01T133L	AATCTACCAATCTGACAAAGGAC	01T133R	TCTTTTGAAGATGTCTGTTCTG	01T133E	TAAACAAATTAACAGAAACAAACAA	01T133A	TGTTTGTGTTTTCTTGTAAATTTGTTAA
01T135L	01T135L	TAAAGTCTTTATGCTTCCAC	01T135R	AGGAATAGATGATGTTGTTCTG	01T135E	GTCACTACGCAATTAACAAATAATCTGATA	01T135A	TATCAGATTAATTTGTAATGGCTGAGTGC
01T137L	01T137L	AAAAAGGAAACGACCTCTCTA	01T137R	AATGGAATCTTAAGTCTGTGA	01T137E	CTTCCGCTGGAGAGGCTGTGTA	01T137A	TACCAAGCTCTTCCAGCGGGAAG
01T138L	01T138L	GAATGATTCACCAATTC	01T138R	AATACCAAGTCTCAGGATGATC	01T138E	GAGATGGAATTAATACACAGCCCTC	01T138A	GAGGGTGTGTTATTAAGTCCATCTC
01T145L	01T145L	GGCAGCTGAGGTTAAGCATCTAA	01T145R	CAGCAGAGTGGGATGATCTGGA	01T145E	CTGGAACACCAATTAAGAAAGCCCTC	01T145A	GTGGCTTTCTATGTTGTTGTTACGG
01T146L	01T146L	ATGTTAGCTCCCACTGTA	01T146R	AGGAAGATGATATCTCTTCCG	01T146E	GCAGAACCAAGTCTGATGAGGAG	01T146A	TCTCAGTACGCTCAATGTTACTTC
01T147L	01T147L	AATATGATGAGCTGATGAAAC	01T147R	TGTGGATGTAAACATATGACT	01T147E	CATTAAGATGATCTCAAGTACTGCCA	01T147A	TGGCAAGTACTGAGATACATCAAGTATG
01T148L	01T148L	AGGAAGATAATAGAGAACTTCA	01T148R	TCTTGATGTGCTGAGCTGACAC	01T148E	GAGTAACTCAATGGCTCATGAGTGC	01T148A	CACTTCACTGCTGGCTGGCAACA
01T150L	01T150L	TCAGAGAAATCGTTGACCTCG	01T150R	TTATGATGATGCTCTCTCTG	01T150E	TGTGCCAGGCCAGAGTGTAAATGG	01T150A	CACTTCACTGCTGGCTGGCAACA
01T151L	01T151L	GTACATGGCCCCCTTTTATC	01T151R	GCCAGAGGCCAGAGGAA	01T151E	CCCTGTGTTGTGCGACCCCTAGGGA	01T151A	TCCCTAGGCTGCAACACACAGG
01T152L	01T152L	TCTCTTAAGCTCATCTGCTTG	01T152R	ACAAATTTTAAACTCCCTTTGGA	01T152E	AQAAAGTCTTTGAAAGAGCTACCTG	01T152A	CAGGTACGCTTTTCAAGAGACTTTCT
01T153L	01T153L	ACTGATATGCTCCAGTAT	01T153R	GAAGTGCAGACAGGATTCAT	01T153E	TTTATATGCCCCCTTTTATGCTATATAACATA	01T153A	TATGTTTATATAGCATAAAGGGCAATATAA
01T154L	01T154L	CCATTTCTCCGTTAAATAA	01T154R	TCTCTTGAAGGTCAAGTCTTTA	01T154E	GAATAATGATTAATGTTCTCAACATAATTCG	01T154A	CGATTAGTGTGAAACACATTAATACATTTC
01T155L	01T155L	GGATAACCTGATGAATTCAAAC	01T155R	AGGGGAATGGGATATCTCG	01T155E	CTGAGTATCCATTTCTTATCTGCTTATCAA	01T155A	TTGAAATAGCAGATAAGGAATGGATCTCAG
01T156L	01T156L	TCTCTCCCTGCTGTTGGGCTT	01T156R	GAGCAATCTTTTGAACAACT	01T156E	ACTGGCCTGATGGAATATGATGG	01T156A	CCAATCAATATCCATCAAGCCCACT
01T157L	01T157L	AGCATGTTCCGATTTTCACTG	01T157R	TATACCATGTAGGTTAGAGAGGGC	01T157E	GAATGTGATGATGAGGAAGGAAGACCA	01T157A	TGCTCTCTCTTTCTCTACTCATCATTC
01T159L	01T159L	GTGAGTATTTGGCTCTCTGA	01T159R	ACTTCCGCTCTGAGAGCTT	01T159E	CCTCAGTAAATGTGGCATTAATAAGTT	01T159A	AATTTAATAATGCCACAAATTAACGTGAGG
01T160L	01T160L	CCCTATATGTCACCAAACT	01T160R	ATATTTTGAAGGCGCAACAG	01T160E	AGATCAAAAGTATTTAAGCTGATTAATAA	01T160A	TTTTAGTTATTCAGTTTAAATATCTTTGATCT
01T162L	01T162L	AATAGGTTTGAAGAGGAAATAG	01T162R	TCATTAAATAATCCCTTGCA	01T162E	GAACAAATATGATGTTGATGATGATGATGCT	01T162A	AGCATAGTTACTATACAGACTAATTTGTTTC
01T164L	01T164L	TAACTGTTCAAGTTAAGTCC	01T164R	TGAAGAGAAAGCTTGAGGAGT	01T164E	GGCAGTTCAAGTGCACAGCTTCA	01T164A	TCTGAGGCTCTGAGCTTATGAGCTCC
01T166L	01T166L	ACATTTCTTTTCCATGTTGAT	01T166R	TCCATACATAGTATTTTCCCA	01T166E	ATTTATGACTCTCTCTTCAATAAGCC	01T166A	GGCATTTTAAAGAGGAGGATCAATTAAT
01T167L	01T167L	CAAAATTTTAAATGCTCTGTGGA	01T167R	AATAGGAAGCTCAAGGACTCAG	01T167E	CCGCTTATGTTGTTTCTTATGTTTATG	01T167A	CATAAAACATTAACAACTAAAGGCGG
01T169L	01T169L	CATACACCTCCCAAGCTAA	01T169R	TTGACTGTAAATCCATCTGTGTC	01T169E	GGAGATCAAAATCTCTACTAGACCAATAACA	01T169A	TGTTATGCTGATGAGGAATTTGATCTCC
01T171L	01T171L	GCAGAGGTGAAGAGGAAAGTGGC	01T171R	TCTTGATGATGCTCTCCAGTTAT	01T171E	AGAGCTGTTTCACTTCTGAGGCTG	01T171A	CAGCCATGATGAGGAAGGAGCTCT
01T172L	01T172L	ACACTCCAGGCTGATGACTCTGG	01T172R	TCTTGATATCACTTGGAGTTAAT	01T172E	TGCTGATGATGAGGAGGAGTGG	01T172A	CCACACTGCTCTTGTCAAGCTGCA
01T173L	01T173L	TTATAGAGATCCCAATGAGCATG	01T173R	ATTACTGTGGTGCACAAAT	01T173E	CACAAATATGGAATCTTCTTGGCTGA	01T173A	TCAGCAGAAAGTCTCTTAATTTTGTG
01T174L	01T174L	AGACAGTCACTGATCTCTCC	01T174R	AATACGCACTCTGAAATTA	01T174E	GAGTACTGATGAGGAGGCTTCAATAG	01T174A	CTTATGAAGCTCTCTCTTATCAAGTACTC
01T176L	01T176L	CAGCTGAGGCAATTAATTCAT	01T176R	AGTGAAGTGAAGGAGGAGTCACT	01T176E	TGGGGGGGTTGGTCCAGAGTGGC	01T176A	GCCATCTTGAGACCAACCCGCCCA
01T178L	01T178L	CCTGTTAATAGCACTACCTCTTT	01T178R	CATCAGAAAGTACCAAGTACATTC	01T178E	CTGTGTAACAATCTCTCAAGTTTCTATG	01T178A	CCATAAATGAATCACTGAGGATTTAACAGC
01T180L	01T180L	TACCAGATTTGAGGCTCAATATCTA	01T180R	ACATAACAAGTTGGTGGTGGT	01T180E	CTTCTGAGCTGGGAGTGTGCAATCC	01T180A	GGATTCTCACTCCAGCTCTCAGAG

Table II

SNP	Name	Left Primer		Right Primer		Labeled Probe		Probe on Slide	
		Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name
01T182L	01T182L	CATGCTTTTGTGAGGAGGCAATC	01T182R	AGGTGCTCAAGTGAAGAGACAA	01T182E	GGCTCTCCAAAAGAGCTATCACTCTCT	01T182A	AGGAAGTGTATGCTCTTTTGGGAGACGC	
01T184L	01T184L	ACCGAGCTAGGCAATGCGAC	01T184R	TCCATTCACCTGAAATTCCTATC	01T184E	CTCCACTGGCAGCTCCCACTATG	01T184A	CATAGTGGGAGCTTGGCCAGTCCAG	
01T185L	01T185L	TTCAATTTGTAGATCTGCTCCCTC	01T185R	CTAATGGGAGTCCATCTCTCT	01T185E	TCATTTGGCAGTGGGTGCTGATGGCC	01T185A	CCCAATCGAACCCAGTGGCAATAGA	
01T187L	01T187L	GTGCAATGTGCTGCTGCTGCTCT	01T187R	CTCCCAAGAAAGAACTCACTCT	01T187E	CTTAAAGCTATCGATCCACCCACTGG	01T187A	CCAGTGGGTGAGTCACTAGCTTAGG	
01T188L	01T188L	TAAAGCTGTAAAGTAACTCTCTC	01T188R	TGAATTTGTGGCTTGACAAA	01T188E	GGCTCTGGGTATAGATTTTGGCACTA	01T188A	TAGTGGCAAACTCTATGACCCAGGCC	
01T189L	01T189L	CAAAGATGCTGCTATTGCAAC	01T189R	CAGATTTGAGCTCTCTCTATCC	01T189E	GGCCAGAGTTTCTGCTTAAGAAATCTTTT	01T189A	AAAGAAATTTCTAGACGAACACTTGGCC	
01T192L	01T192L	AAACATTTTAGAGGCCAAGT	01T192R	TAAATTTGAGCTCTCAAAAGCCG	01T192E	CCGCAATCTATCTATGAAGATATGCTGG	01T192A	GCTAAATTTGCTATGAAGATATGCTGG	
01T194L	01T194L	AAGACTCTGAAGCACCAGTATC	01T194R	TCTTGAATTTGGCAATGGCTTG	01T194E	AGCAATGGCAACAGTGGAGAGATA	01T194A	TATCTCTCTGAGTGTCTCATGCT	
01T195L	01T195L	TGAAGGAGTGGCTGCTGCTCAAT	01T195R	CTTACATGAAATTTATGCTCTCAT	01T195E	CACATTTTCAAGAAATACATATTTTAAAGA	01T195A	TCTTAAATTTTATGATTTTGTGGAAAGTGG	
01T196L	01T196L	GTCAAAATCTTGTATGCTT	01T196R	ATCTCTGTGCTATGGAGGTAG	01T196E	TGAGAAATATTTGCTGTATTAAGCTGTGT	01T196A	AAACAGGTTTATACAGCAAAATATCTTAC	
01T200L	01T200L	TTTACATGATGATGACCAACAA	01T200R	TTTACGCTGTGGGATATATAG	01T200E	CATCATAGATTAAGGCCAAATATGCA	01T200A	TGCATATTTGGCTTAATACTCTATGATG	
01T202L	01T202L	CTTTTCAATGCTATGCTATC	01T202R	CTGCTTTTCCACTTGTATC	01T202E	CTCTCACTATTAAACAAATATGAGGATA	01T202A	AAATGATTCAGGAAATATGCTGTATTAACA	
01T205L	01T205L	AGTGGCTTTCAAGATCTCTT	01T205R	GCCAGATAGCTGCAATGATTAATA	01T205E	TTTGTCTTGAATTCACAGATTTAAT	01T205A	AAATAACTGTGAAATCCCAAGACAAA	
01T206L	01T206L	AGATGCTGACCAAGCTTAAACT	01T206R	TGAGCTGTGTGAGCCACTCT	01T206E	TAACTCAAACTGAGGAAAGGCCCA	01T206A	TGCCCCCTCTCTCAGTTTGTATTA	
01T207L	01T207L	TGGCTATTTTGTGATCAAAAT	01T207R	ACTGCTGAGCAATGACATCTCTCT	01T207E	TCCTGTGATCACGGACTATTAATCT	01T207A	AGATTAATATAGTCTGTGTGATCAAGGA	
01T208L	01T208L	AATCGAGAGCAATGCTAGT	01T208R	TGGCAAGAGCAAGCACTTCT	01T208E	AATAGAACAGTTTAACTAATCTTAGACTGC	01T208A	GCAGTCAAGTTAAATTAATTAATCTTTCTATT	
01T209L	01T209L	AGATTAATGATGATGCTGCTA	01T209R	AATTTCTCTCAGTGTGACTCA	01T209E	TCACCAAGAACTTAGAGATCTGTCTCT	01T209A	AGAGAAACAGATCTCTAAGTTTCTGTGCA	
01T211L	01T211L	ACCGAGAGGCAATGGAACAT	01T211R	GCCAAAGACTTTGACGGCTTA	01T211E	GATGTGTAGCAATTAATTTTCTTAGGCTA	01T211A	TAGCTTAAGAAACAAATACGTCTACACATC	
01T217L	01T217L	TAAATGAGAAATGACCCAAATG	01T217R	CTCAGGAGCAATATCTCTG	01T217E	GGCCATAGAGGATTAATTTTAACTCTCA	01T217A	TGAGAGTTAATAAATAATCTCTCTATGGGC	
01T220L	01T220L	ATTTTCTTCAATCACTGCTCTC	01T220R	GGCTATGCTGATATCTCAAT	01T220E	CTCTCATCACAGAGTGTCCAACTAGAA	01T220A	TCTAGATTTTGTCACTCTGTGTGTGATGAG	
01T221L	01T221L	CCAAAGGAATGACATATGTTTA	01T221R	GGCTATGCTGATATCTCAAT	01T221E	CCATCTTTATCTCTATTAAGGCCAC	01T221A	GCATTTGGAACCTCTACCTCTGAGC	
01T222L	01T222L	CTCTAGGCTCTCACACATCTCACT	01T222R	AACAGAGGATGAAATATGCTTA	01T222E	CGCTTATCTCTCTATTAAGGCCAC	01T222A	GGTGGCTTAATGAGGATTAAGAAATGG	
01T223L	01T223L	TAGGCAATCTGACATCTGCTT	01T223R	AGAAATGCAATATGCTGCTG	01T223E	AACTTGAAGATTAATCTTTCTCTAC	01T223A	TTGAACTTTCAAGTGTGCTTAAAG	
01T224L	01T224L	CAAAAGCTAAAGGGGCACT	01T224R	GATTCATGATCAATATGCTGCTG	01T224E	GGCTTGAAGATTAATCTTTCTCTAC	01T224A	TGACAGCAAGAAAGAAATATCTCAGTT	
01T228L	01T228L	CGCTAAAGAGGAAAGGCTCTCT	01T228R	CAGGTCTCAGGATGTCAGACACT	01T228E	TGCCCTAGACATCTCTGCGCACT	01T228A	AGTTGGCAGGATGTCTAGGGCA	
01T230L	01T230L	TGAATTTGACTTTTAAATGTTTA	01T230R	CTCAGGAGCAAGCGGCAAA	01T230E	GGCCATGAAAGCGCCAAAGAGG	01T230A	TAGTTTGTGCTCTTTTAACTGTGGCC	
01T231L	01T231L	TTTTCAGGATGATATCTGCTCTA	01T231R	CAATCTCTCCAGGCTCTCCCA	01T231E	AAATATTAATAGTCACTATATGGTACGTG	01T231A	CTCTTTTGGCTCTCTTAACTGTGGCC	
01T232L	01T232L	ACCATGAAATAGATGACAGATGAG	01T232R	ATCCTTTGATGATCCCTCAAAATA	01T232E	CCATAGGGGTGAGTGGCAAGAAATTTG	01T232A	CAGTATGCCATATAGTGTACTATATATTT	
01T233L	01T233L	GGGAGGTGTGAGGGGAGGGGCA	01T233R	AAATGGTAAAGAAATTTTGTCTTA	01T233E	ATGGAGACACATCTCATCTCTCTCC	01T233A	CAATTTCTTGGCACTCACCTCTTGG	
01T234L	01T234L	GGCTATGCTACAGTCTCTAGCTAA	01T234R	AAAGAGCTGAAAGTCCCAAT	01T234E	CAGTTTGTGCTGCTATGTTGTCTCTC	01T234A	GGAGAGGATGAATGTGCTCTTCCAT	
01T236L	01T236L	TCTCTGTGGGAGCACTGTCTCAGTG	01T236R	GAGAGTGGGCACTGTCACTCTCT	01T236E	GTGGCTCTGATCTAGGGCTTGGGCC	01T236A	GAAGACTCAACAATGCACTGCAACACTG	
01T237L	01T237L	AAAGGCTATGAGGATGCAACAA	01T237R	TGCCAATGCTCTCTCCCAACT	01T237E	GTGGCTCTGATCTAGGGCTTGGGCC	01T237A	GCCTCAAGCTAGATCAGAGGCCAC	
01T240L	01T240L	GGCTGAAAGGATGATGATTTTA	01T240R	TGGGTGATCAAGTCTGCTCAG	01T240E	GAGGCTCAGAGGGGCCAGAGCTGA	01T240A	TCACCTCTGGCCCTGTGAGGCTC	
01T241L	01T241L	TGCTTATGTGCTCTTTTCACTC	01T241R	CATCTGATCTCTCTATACCTCA	01T241E	CAATATAGGGTGAATAGTCTCTGACA	01T241A	AGGTTAGATTTTTTTTATGAAATAGCAAT	
01T242L	01T242L	ATTGATCATCTCAATGCTA	01T242R	TGGTCCAATGAACTGGGCAAAA	01T242E	CAGTGGGGCTGCTATGCTCTAT	01T242A	TGTAGATGAACATTAACAGCTCTATATG	
01T244L	01T244L	TGGAAGGAGCTGTCTCTCTGCTG	01T244R	GAGGCCCTGAGTGTGAGGATGAG	01T244E	CAGTGGGGCTGCTATGCTCTAT	01T244A	ATGAGGCCATGCAAGCCCTCCACTG	
01T246L	01T246L	CCTTCCCAATTAAGGACTCT	01T246R	GACATCTGCAATATCCCAAGT	01T246E	GGCAAGATTTTTTAAAGACATGAAAG	01T246A	TGCACAGATTAACGTCTATCTGCTGAGTCC	
01T247L	01T247L	AAGAAATGAAATGAAAAACAGTA	01T247R	TGATTTTGTCAATACCTTAGCAT	01T247E	ATAATGATGGCAAGCTTAAGGAGGAG	01T247A	CTCCTCTTACCTTGGCATCTATAT	
01T248L	01T248L	GTCTGGAGGCTCACTGCTGAG	01T248R	ACGTGACACATTAATCCCAAGT	01T248E	GTGATACATATGAGCTTAATGCAATGGT	01T248A	ACCATGTTTGGCAATAGCTCATATGTTATCAC	
01T249L	01T249L	TGGCTCTACTTCAAAAGTCTT	01T249R	AAATCTGAAACCTGTGGAA	01T249E	GGCAAGATTTTTTAAAGACATGAAAG	01T249A	CTTTCTATGCTTTTAAAAAATCTTCCC	
01T250L	01T250L	ATACCAATCTATCAAGAAAGCGC	01T250R	GGCGGGGCGAGGGTAAAGTGTGA	01T250E	CTGCTTTTGTTCATTTTGTCTTAAACA	01T250A	TGTTTAAGGCAAAATGAAACAAACAGG	
01T251L	01T251L	AAAGTGTATGCTCAATATGCG	01T251R	TCCAGCAATGTCTCTGCTGGTAG	01T251E	CTGCTGAGTGTCTATGCTTGTGATTTCT	01T251A	AGAAATCAAGAGCTAATAGCACTACCCAGG	
01T253L	01T253L	TCCTCAGAAATCTCCAAACACC	01T253R	GGAAGAGCTGGCCCATGATTC	01T253E	GGCAAGATTTTTTAAAGACATGAAAG	01T253A	TGCTGCAAAAGTCAAGCTGTGTTTGGCC	
01T255L	01T255L	TTCTCAGAAATCTCCAAACACC	01T255R	TAAGGAGCTGAGGATGCTCT	01T255E	TGCCCTCAGGAAATACAAAGAAAT	01T255A	ATCTTGTATCTCTCTGAGGGCA	
01T256L	01T256L	CTTTGTGTATGCTGAGCAAC	01T256R	AATCTCTACTGTCTCTGAC	01T256E	CCGCTCTCTTAAAAAAAATCTATTTA	01T256A	TAAAGATGATTTTTTTTTTAAAGCTGAGCCGCG	
01T257L	01T257L	CTACTAGAGGATGAGGCACTCAAA	01T257R	ACACACTGCTCACTCTCTG	01T257E	CCGCACTAAAAACCGTAAAGATGAA	01T257A	AGCATTAATTTAGGAAATATAAGACATCTCG	
01T258L	01T258L	CAGTAAAGGATGAGGCACTCAAA	01T258R	ATTCGCACTGCTCACTCTG	01T258E	CCGCACTAAAAACCGTAAAGATGAA	01T258A	TTTACTCTAGGGTTTTAGTGGGG	
01T259L	01T259L	TCAACTGTGCTATATATGAGG	01T259R	CCTTAGGTGTCTCTCTGGTA	01T259E	GCTCAGAGATTAAGTCTCTGAGAACTCTCT	01T259A	AGAGGTTTCTAGGGGAGACTAATCTGAGC	
01T262L	01T262L	AGAGGCACTTTCCCACTGCTTGA	01T262R	TAGATCTAGGCCATATGACATAG	01T262E	CACATACATCTCTATTAAGTTATCCAAAG	01T262A	CTTTGGATACTTATTAATGGATGATATGTCG	
01T266L	01T266L	GGCTGAGACTGTCTGCTAA	01T266R	TCTTCCCTGTGTGTGATTAAT	01T266E	CTAGAACACACAACTCCACTCAAGTA	01T266A	TACTGTAAAGGTGGAATTTGTGTTCTTAG	
01T267L	01T267L	TAGAACACACTGCTCCGCAAT	01T267R	AGCAACTGGGGGCGGGGCGCAATG	01T267E	AAGAAATGAGGTTTCCACGCGGGAGC	01T267A	GCCTCCGCGGTGGAACTCTATCTT	

Table II

SNP	Name	Left Primer		Right Primer		Labeled Probe		Probes on Slide	
		Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name
01T268I	01T268L	TTGTGCTGATGATTAATCTTA	01T268R	TGATCAGAAGCACATCTTTTA	01T268E	CACTGCACATCTCTATGCAATGTAACAAA	01T268A	TTTGTACATGCAATGATGTCAGTG	01T268I
01T270I	01T270L	GGGACATGTGCTTGCACACCG	01T270R	CAATACAGTCCCTCCATCTCTAGT	01T270E	CCACTAGTACTCTCATTTAGTCCCTGGAA	01T270A	TTCCAGGCACTAAATGGAATGATGATGG	01T270I
01T271I	01T271L	ATTGAGAGAGAAAGAACAAAGT	01T271R	GTAAGCTCCAGTGGGTGAC	01T271E	TAAAGGTGCCAAGAGCCCTGCAATC	01T271A	GATTCAGGCTCTTGGCAGCTGTTA	01T271I
01T272I	01T272L	CTGACTCTCTTCCCTCAACAT	01T272R	TCAATTAATTTGGCTAGATGGTA	01T272E	GATCAGGCTTTCCTCATTTAAAGTAAT	01T272A	ATTACTTTAAATGGGAAGGCTTGATC	01T272I
01T273I	01T273L	CCGAGAAACCTTAAATATAGACAG	01T273R	TTTAAATGTCTCTCTCTGACT	01T273E	GGAAGCCAAAATAGGAATAAAAGATC	01T273A	GATCTTTTATTTCTCTATTTTGGCTCC	01T273I
01T274I	01T274L	CAAACTTGAAGGATCTATCT	01T274R	TTCTCCCTATCTCTCCCTTA	01T274E	GTCTCTCATCTGATCTCTACAAAGTAA	01T274A	TTACCTTTTGAGCAAGAAATCAGCAGC	01T274I
01T275I	01T275L	CCAGGCCCCAGAAAGACGGCTGG	01T275R	GGCAGAGTGTCTTTTGGCAAT	01T275E	GTCTGCTACTGTCTCAATGAGGCCATA	01T275A	TTATGGCTCTCATTTGAACATGACGAGC	01T275I
01T276I	01T276L	GGTGAATCAGGAAGATTTCTAAAGT	01T276R	CTCTCTCGAAGTCTGTAGGAG	01T276E	CTTCTTAATCTGCTTAATGCTTTAGTTGAG	01T276A	CTACAATCAAGCATTTAGCGATTAAAGGAAG	01T276I
01T277I	01T277L	CCCTGCTGTGCTCTCTCTCTG	01T277R	GGTTTGGCATGCGGTCTCGA	01T277E	CTCTAGCTATGATCTCAATCTGCTCC	01T277A	GGACCAAGTGGAGGTAAATGAAATCAGAGG	01T277I
01T278I	01T278L	ACCTACAGATCTCATGAGACT	01T278R	TACAGTTTCCCAACAAAATAA	01T278E	AGAGTATAGATAGGTGTGAAGGATGG	01T278A	CCATCTCTCACACCTATCTCTACTCT	01T278I
01T279I	01T279L	AGGCTGCCATTTCTTAATC	01T279R	TCCACCCCTGGGCTGCTTC	01T279E	CGCGCCGCGAGCATGGGATCTG	01T279A	TCGCTCTCAGGTGTATTCTCTCTCTG	01T279I
01T280I	01T280L	CGGTTTATGCAATCTCTCAAA	01T280R	CTGCGGCACTTTCTTAATGAT	01T280E	GTGCTCTCAGGCTTTTCAACCATAT	01T280A	AAATGTTTGAAGGTGGGTGAAGAGCAG	01T280I
01T281I	01T281L	GGTACCAAGATTTCCAAATCAAT	01T281R	TATACCTTTCTCTCCCAATCT	01T281E	CAAGAGAAGAAATAAAGCTTTTTCAGAG	01T281A	CTCTGAAAAGGTATTATTTCTCTCTG	01T281I
01T282I	01T282L	GTGAGCAATTTCAAGATCTTCTCA	01T282R	TTCTCTGATTAATGAGCATCT	01T282E	ATATAAATAGTAAGTATTTTAAATAGAGTT	01T282A	AATCTCTATTTTAAATCTTCTTATTTAT	01T282I
01T283I	01T283L	GTATGCTCATTTAAACATTTATTCG	01T283R	GAAATGCAAAATTTTAAAGCTGATTC	01T283E	CATATTTCCATTTGATGATAAAATATCTTAA	01T283A	TTAAGAGATTTTATTCGAATGGAATATG	01T283I
01T284I	01T284L	CCCAATCAAAATGATCACTCACT	01T284R	TTCTTCAACCAATATGTTG	01T284E	CCAAGCTTATCTGTGTTTCTTCTTA	01T284A	TAAAGCAATGAACACAGATACACCTTCC	01T284I
01T285I	01T285L	CTATGCTGCTCTTCCCAATTTAC	01T285R	GAAATGACCTGGGCAATGCACTAA	01T285E	CCAGGTGAAATGGCTGCAAGGT	01T285A	ACCTGTGACCAATTTTCAACCTGG	01T285I
01T286I	01T286L	ACCTGAAAGAAAGAAATCACT	01T286R	TGCACATGTACCAATTTCTTT	01T286E	ATTATCCACTGATGGGCACTTCGG	01T286A	CCGAAAGTCCCATCATGCTGGATGAAT	01T286I
01T287I	01T287L	TTCTGTTTCCAGCACTTAAAGT	01T287R	TGCTATGATCTAGCAATCAAGT	01T287E	GTGTTAGTGTGAAGAAATGTTCTCA	01T287A	TTATCTCTAAAAGCAAAAGTTTCAAGCTGGG	01T287I
01T288I	01T288L	CAATAATACAGCTGCCACAGCC	01T288R	TTTGTAGTAAGTAAGTATCAAC	01T288E	CCCACTCTGAACTTTTCTTTTGGAGTAA	01T288A	CTCTAGCAGGAACTCAATTAAGAGCCC	01T288I
01T289I	01T289L	CAATAATACAGCTGCCACAGCC	01T289R	TGCTATGATCTAGCAATCAAGT	01T289E	GGGCTCTTATGATCTGCTCTAAGAC	01T289A	TTGCTCTCTCTCTCTCTCCCACT	01T289I
01T290I	01T290L	CAATAATACAGCTGCCACAGCC	01T290R	GTGTTTAAATCACTACTCTGG	01T290E	AGTGTGGAGAGAGAGGGGAGCA	01T290A	TTGCTCTCTCTCTCTCTCCCACT	01T290I
01T291I	01T291L	CAATAATACAGCTGCCACAGCC	01T291R	ATCCATGAAATTTTCTTCTTAT	01T291E	AGTGTGGAGAGAGAGGGGAGCA	01T291A	TTGCTCTCTCTCTCTCTCCCACT	01T291I
01T292I	01T292L	CAATAATACAGCTGCCACAGCC	01T292R	AACATAAGCAAGCAAGCTTCA	01T292E	CTCTGCTGCGAGACTCTCTTTATCTCT	01T292A	AGAGATAAGGAAGTCTGGCAGCAGC	01T292I
01T293I	01T293L	CAATAATACAGCTGCCACAGCC	01T293R	CTCTAGCACTGCTGCT	01T293E	CGTCTGCGCAGACTCTCTTTATCTCT	01T293A	AGTCAAGTACTTGTACTTAATCAACCG	01T293I
01T294I	01T294L	CAATAATACAGCTGCCACAGCC	01T294R	AGGCACTTCTGTAAGTATG	01T294E	CGTCTGCGCAGACTCTCTTTATCTCT	01T294A	AGTCAAGTACTTGTACTTAATCAACCG	01T294I
01T295I	01T295L	CAATAATACAGCTGCCACAGCC	01T295R	AGGCACTTCTGTAAGTATG	01T295E	CGTCTGCGCAGACTCTCTTTATCTCT	01T295A	AGTCAAGTACTTGTACTTAATCAACCG	01T295I
01T296I	01T296L	CAATAATACAGCTGCCACAGCC	01T296R	AGGCACTTCTGTAAGTATG	01T296E	CGTCTGCGCAGACTCTCTTTATCTCT	01T296A	AGTCAAGTACTTGTACTTAATCAACCG	01T296I
01T297I	01T297L	CAATAATACAGCTGCCACAGCC	01T297R	AGGCACTTCTGTAAGTATG	01T297E	CGTCTGCGCAGACTCTCTTTATCTCT	01T297A	AGTCAAGTACTTGTACTTAATCAACCG	01T297I
01T298I	01T298L	CAATAATACAGCTGCCACAGCC	01T298R	AGGCACTTCTGTAAGTATG	01T298E	CGTCTGCGCAGACTCTCTTTATCTCT	01T298A	AGTCAAGTACTTGTACTTAATCAACCG	01T298I
01T299I	01T299L	CAATAATACAGCTGCCACAGCC	01T299R	AGGCACTTCTGTAAGTATG	01T299E	CGTCTGCGCAGACTCTCTTTATCTCT	01T299A	AGTCAAGTACTTGTACTTAATCAACCG	01T299I
01T300I	01T300L	CAATAATACAGCTGCCACAGCC	01T300R	AGGCACTTCTGTAAGTATG	01T300E	CGTCTGCGCAGACTCTCTTTATCTCT	01T300A	AGTCAAGTACTTGTACTTAATCAACCG	01T300I
01T301I	01T301L	CAATAATACAGCTGCCACAGCC	01T301R	AGGCACTTCTGTAAGTATG	01T301E	CGTCTGCGCAGACTCTCTTTATCTCT	01T301A	AGTCAAGTACTTGTACTTAATCAACCG	01T301I
01T302I	01T302L	CAATAATACAGCTGCCACAGCC	01T302R	AGGCACTTCTGTAAGTATG	01T302E	CGTCTGCGCAGACTCTCTTTATCTCT	01T302A	AGTCAAGTACTTGTACTTAATCAACCG	01T302I
01T303I	01T303L	CAATAATACAGCTGCCACAGCC	01T303R	AGGCACTTCTGTAAGTATG	01T303E	CGTCTGCGCAGACTCTCTTTATCTCT	01T303A	AGTCAAGTACTTGTACTTAATCAACCG	01T303I
01T304I	01T304L	CAATAATACAGCTGCCACAGCC	01T304R	AGGCACTTCTGTAAGTATG	01T304E	CGTCTGCGCAGACTCTCTTTATCTCT	01T304A	AGTCAAGTACTTGTACTTAATCAACCG	01T304I
01T305I	01T305L	CAATAATACAGCTGCCACAGCC	01T305R	AGGCACTTCTGTAAGTATG	01T305E	CGTCTGCGCAGACTCTCTTTATCTCT	01T305A	AGTCAAGTACTTGTACTTAATCAACCG	01T305I
01T306I	01T306L	CAATAATACAGCTGCCACAGCC	01T306R	AGGCACTTCTGTAAGTATG	01T306E	CGTCTGCGCAGACTCTCTTTATCTCT	01T306A	AGTCAAGTACTTGTACTTAATCAACCG	01T306I
01T307I	01T307L	CAATAATACAGCTGCCACAGCC	01T307R	AGGCACTTCTGTAAGTATG	01T307E	CGTCTGCGCAGACTCTCTTTATCTCT	01T307A	AGTCAAGTACTTGTACTTAATCAACCG	01T307I
01T308I	01T308L	CAATAATACAGCTGCCACAGCC	01T308R	AGGCACTTCTGTAAGTATG	01T308E	CGTCTGCGCAGACTCTCTTTATCTCT	01T308A	AGTCAAGTACTTGTACTTAATCAACCG	01T308I
01T309I	01T309L	CAATAATACAGCTGCCACAGCC	01T309R	AGGCACTTCTGTAAGTATG	01T309E	CGTCTGCGCAGACTCTCTTTATCTCT	01T309A	AGTCAAGTACTTGTACTTAATCAACCG	01T309I
01T310I	01T310L	CAATAATACAGCTGCCACAGCC	01T310R	AGGCACTTCTGTAAGTATG	01T310E	CGTCTGCGCAGACTCTCTTTATCTCT	01T310A	AGTCAAGTACTTGTACTTAATCAACCG	01T310I
01T311I	01T311L	CAATAATACAGCTGCCACAGCC	01T311R	AGGCACTTCTGTAAGTATG	01T311E	CGTCTGCGCAGACTCTCTTTATCTCT	01T311A	AGTCAAGTACTTGTACTTAATCAACCG	01T311I
01T312I	01T312L	CAATAATACAGCTGCCACAGCC	01T312R	AGGCACTTCTGTAAGTATG	01T312E	CGTCTGCGCAGACTCTCTTTATCTCT	01T312A	AGTCAAGTACTTGTACTTAATCAACCG	01T312I
01T313I	01T313L	CAATAATACAGCTGCCACAGCC	01T313R	AGGCACTTCTGTAAGTATG	01T313E	CGTCTGCGCAGACTCTCTTTATCTCT	01T313A	AGTCAAGTACTTGTACTTAATCAACCG	01T313I
01T314I	01T314L	CAATAATACAGCTGCCACAGCC	01T314R	AGGCACTTCTGTAAGTATG	01T314E	CGTCTGCGCAGACTCTCTTTATCTCT	01T314A	AGTCAAGTACTTGTACTTAATCAACCG	01T314I
01T315I	01T315L	CAATAATACAGCTGCCACAGCC	01T315R	AGGCACTTCTGTAAGTATG	01T315E	CGTCTGCGCAGACTCTCTTTATCTCT	01T315A	AGTCAAGTACTTGTACTTAATCAACCG	01T315I
01T316I	01T316L	CAATAATACAGCTGCCACAGCC	01T316R	AGGCACTTCTGTAAGTATG	01T316E	CGTCTGCGCAGACTCTCTTTATCTCT	01T316A	AGTCAAGTACTTGTACTTAATCAACCG	01T316I
01T317I	01T317L	CAATAATACAGCTGCCACAGCC	01T317R	AGGCACTTCTGTAAGTATG	01T317E	CGTCTGCGCAGACTCTCTTTATCTCT	01T317A	AGTCAAGTACTTGTACTTAATCAACCG	01T317I
01T318I	01T318L	CAATAATACAGCTGCCACAGCC	01T318R	AGGCACTTCTGTAAGTATG	01T318E	CGTCTGCGCAGACTCTCTTTATCTCT	01T318A	AGTCAAGTACTTGTACTTAATCAACCG	01T318I
01T319I	01T319L	CAATAATACAGCTGCCACAGCC	01T319R	AGGCACTTCTGTAAGTATG	01T319E	CGTCTGCGCAGACTCTCTTTATCTCT	01T319A	AGTCAAGTACTTGTACTTAATCAACCG	01T319I
01T320I	01T320L	CAATAATACAGCTGCCACAGCC	01T320R	AGGCACTTCTGTAAGTATG	01T320E	CGTCTGCGCAGACTCTCTTTATCTCT	01T320A	AGTCAAGTACTTGTACTTAATCAACCG	01T320I
01T321I	01T321L	CAATAATACAGCTGCCACAGCC	01T321R	AGGCACTTCTGTAAGTATG	01T321E	CGTCTGCGCAGACTCTCTTTATCTCT	01T321A	AGTCAAGTACTTGTACTTAATCAACCG	01T321I
01T322I	01T322L	CAATAATACAGCTGCCACAGCC	01T322R	AGGCACTTCTGTAAGTATG	01T322E	CGTCTGCGCAGACTCTCTTTATCTCT	01T322A	AGTCAAGTACTTGTACTTAATCAACCG	01T322I
01T323I	01T323L	CAATAATACAGCTGCCACAGCC	01T323R	AGGCACTTCTGTAAGTATG	01T323E	CGTCTGCGCAGACTCTCTTTATCTCT	01T323A	AGTCAAGTACTTGTACTTAATCAACCG	01T323I
01T324I	01T324L	CAATAATACAGCTGCCACAGCC	01T324R	AGGCACTTCTGTAAGTATG	01T324E	CGTCTGCGCAGACTCTCTTTATCTCT	01T324A	AGTCAAGTACTTGTACTTAATCAACCG	01T324I
01T325I	01T325L	CAATAATACAGCTGCCACAGCC	01T325R	AGGCACTTCTGTAAGTATG	01T325E	CGTCTGCGCAGACTCTCTTTATCTCT	01T325A	AGTCAAGTACTTGTACTTAATCAACCG	01T325I
01T326I	01T326L	CAATAATACAGCTGCCACAGCC	01T326R	AGGCACTTCTGTAAGTATG	01T326E	CGTCTGCGCAGACTCTCTTTATCTCT	01T326A	AGTCAAGTACTTGTACTTAATCAACCG	01T326I
01T327I	01T327L	CAATAATACAGCTGCCACAGCC	01T327R	AGGCACTTCTGTAAGTATG	01T327E	CGTCTGCGCAGACTCTCTTTATCTCT	01T327A	AGTCAAGTACTTGTACTTAATCAACCG	01T327I
01T328I	01T328L	CAATAATACAGCTGCCACAGCC	01T328R	AGGCACTTCTGTAAGTATG	01T328E	CGTCTGCGCAGACTCTCTTTATCTCT	01T328A	AGTCAAGTACTTGTACTTAATCAACCG	01T328I
01T329I	01T329L	CAATAATACAGCTGCCACAGCC	01T329R	AGGCACTTCTGTAAGTATG	01T329E	CGTCTGCGCAGACTCTCTTTATCTCT	01T329A	AGTCAAGTACTTGTACTTAATCAACCG	01T329I
01T330I	01T330L	CAATAATACAGCTGCCACAGCC	01T330R	AGGCACTTCTGTAAGTATG	01T330E	CGTCTGCGCAGACTCTCTTTATCTCT	01T330A	AGTCAAGTACTTGTACTTAATCAACCG	01T330I
01T331I	01T331L	CAATAATACAGCTGCCACAGCC	01T331R	AGGCACTTCTGTAAGTATG	01T331E	CGTCTGCGCAGACTCTCTTTATCTCT	01T331A	AGTCAAGTACTTGTACTTAATCAACCG	01T331I
01T332I	01T332L	CAATAATACAGCTGCCACAGCC	01T332R	AGGCACTTCTGTAAGTATG	01T332E	CGTCTGCGCAGACTCTCTTTATCTCT	01T332A	AGTCAAGTACTTGTACTTAATCAACCG	01T332I
01T333I	01T333L	CAATAATACAGCTGCCACAGCC	01T333R	AGGCACTTCTGTAAGTATG	01T333E	CGTCTGCGCAGACTCTCTTTATCTCT	01T333A	AGTCAAGTACTTGTACTTAATCAACCG	01T333I
01T334I	01T334L	CAATAATACAGCTGCCACAGCC	01T334R	AGGCACTTCTGTAAGTATG	01T334E	CGTCTGCGCAGACTCTCTTTATCTCT	01T334A	AGTCAAGTACTTGTACTTAATCAACCG	01T334I
01T335I	01T335L	CAATAATACAGCTGCCACAGCC	01T335R	AGGCACTTCTGTAAGTATG	01T335E	CGTCTGCGCAGACTCTCTTTATCTCT	01T335A	AGTCAAGTACTTGTACTTAATCAACCG	01T335I
01T336I	01T336L	CAATAATACAGCTGCCACAGCC	01T336R	AGGCACTTCTGTAAGTATG	01T336E	CGTCTGCGCAGACTCTCTTTATCTCT	01T336A	AGTCAAGTACTTGTACTTAATCAACCG	01T336I
01T337I	01T337L	CAATAATACAGCTGCCACAGCC	01T337R	AGGCACTTCTGTAAGTATG	01T337E	CGTCTGCGCAGACTCTCTTTATCTCT	01T337A	AGTCAAGTACTTGTACTTAATCAACCG	01T337I
01T338I	01T338L	CAATAATACAGCTGCCACAGCC	01T338R	AGGCACTTCTGTAAGTATG	01T338E	CGTCTGCGCAGACTCTCTTTATCTCT	01T338A	AGTCAAGTACTTGTACTTAATCAACCG	01T338I
01T339I	01T339L	CAATAATACAGCTGCCACAGCC	01T339R	AGGCACTTCTGTAAGTATG	01T339E	CGTCTGCGCAGACTCTCTTTATCTCT	01T339A	AGTCAAGTACTTGTACTTAATCAACCG	01T339I
01T340I	01T340L	CAATAATACAGCTGCCACAGCC	01T340R	AGGCACTTCTGTAAGTATG	01T340E	CGTCTGCGCAGACTCTCTTTATCTCT	01T340A	AGTCAAGTACTTGTACTTAATCAACCG	01T340I
01T341I	01T341L	CAATAATACAGCTGCCACAGCC	01T341R	AGGCACTTCTGTAAGTATG	01T341E	CGTCTGCGCAGACTCTCTTTATCTCT	01T341A	AGTCAAGTACTTGTACTTAATCAACCG	01T341I

[illegible]

Table 11

[illegible]

Table II

SNP	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')	Left Primer	Right Primer
16-0121	16-0121	GTCTGAGTCTGAGTATGTGAT			16-012R	TGCTCATCTCTGTCTGCTA			16-012E	ACCTGTCTTTTGTGGACATCTGCTTCTCT		
16-0131	16-0131	CCCTTCTCTCCCAAGTGGGA			16-013R	CATCCCAAACTACAGAGATCG			16-013E	AGACTCTGCCACCAGAGGTGGGCT		
16-0141	16-0141	ACATCTGTGGAAGTGTGACAA			16-014R	AGTGGTGGCCAGGGTTTGG			16-014E	TGACACTAACTCAGGAGCAACATG		
16-0161	16-0161	CATCACCCTCCAGAGCTGGAG			16-016R	GTGAGTGGGTCTGTGTGGG			16-016E	GTGTGCGGAGGACAGAGATCTCGCT		
16-0171	16-0171	AAATCCCAAGCAACTGAAGCGGC			16-017R	AGCTGTGGTCCCATATATGGTAA			16-017E	AAAGCTGTGGAGGACAGAGATCTCGCT		
16-0181	16-0181	TAATCCCAAGCAACTGAAGCGCTAA			16-018R	TTAGTGAGGAGAGTAGAGCG			16-018E	AAAGCTGTGGAGGACAGAGATCTCTTAATTC		
16-0201	16-0201	TACCTGCACAGCGCATCTCTA			16-020R	AACAGGATGAGCTGCTTAATAGTA			16-020E	TTCTAGACTCTGGCTCTCTTTCCAGGCCAGG		
16-0211	16-0211	TCAGAGAAGCGCTATGCGGC			16-021R	TTGTCTTGATTTCTACTGTAGAC			16-021E	CTGTGTGAAGGTGACCTGTCTTTGTGGAA		
16-0221	16-0221	GGATGCAATGTTTCCCAAC			16-022R	CATCACTGCTATCTTAACTTGT			16-022E	AACATGACTCTGCGAGGTCTAATAGTCT		
16-0231	16-0231	TCTCTCTGTGACTTCTGGAT			16-023R	TTGTGTGCAAAATTTGCCCTGTA			16-023E	TTCATAGACAGCCCGTCTTACAGCCCT		
16-0241	16-0241	AGCGGGGTCTCTCTCATAGT			16-024R	GGAGTGTGCAAAATTTGCCCTTAC			16-024E	ATTAAATGGAGACTGAATGTTGTGGATAC		
16-0251	16-0251	ATCTGTCTCTGTCTACAC			16-025R	GTGAATGAGCTTGTGTGTGTGACA			16-025E	CATCTGGCACCACTTTCCACCCAGCT		
16-0261	16-0261	TCTCCACATAGGGCAAGTG			16-026R	TGGAAATGATGAGGGGTAGTG			16-026E	GAATGTGCCCTTTGTGCAATCAAGC		
16-0281	16-0281	TGCCCAAGCGGCTTACCTAGT			16-028R	CTGTGGCTCTGCAAGGAAGTCC			16-028E	GTCTCTGATGGAATGGAAGTGAAGTT		
16-0311	16-0311	TCCCTCTTAATGTGTCAATG			16-031R	CAAGTGGGAAGGAAGAAATTTCT			16-031E	AAATTCGAAGTCTCTTTTAAAGGAGG		
16-0321	16-0321	TGAGGCACTGTGTGAATCTCT			16-032R	TATACATATCAGAGCGGAA			16-032E	AAATTCGAAGTCTCTTTTAAAGGAGG		
16-0331	16-0331	GCAATCTCTAGAAATTTGGCAT			16-033R	TGAGAAATTTTCCCTCAACAT			16-033E	GGAGCAGGGCTTCACTTTATGTGCTTA		
16-0351	16-0351	CAGCTCAACAGCTGTCCCT			16-035R	CTGTGTGAGCTTGTGTGTGGAAC			16-035E	GTGGGGGAAGAAACAAATCTGTGCAAGC		
16-0371	16-0371	ATGGGCGCATGGGCTTTCTTAC			16-037R	CGCTCTGAGCTGATTTAGGAAC			16-037E	GCTGCTGTGTGCGGCTCTGCTGCAA		
16-0381	16-0381	ACTCCCAAACTCGGTTTGG			16-038R	GAATGAAGTCCGCGAGGTA			16-038E	CTCCCACTGCAAGTGTGTGCTCTGGA		
16-0391	16-0391	TTCGCTCTGGAGTTTACAGTTGG			16-039R	TATTTCTTCACTGCCCTTAGTAT			16-039E	TAGTATATCTGAAACGCTTATTAATCTCTG		
16-0401	16-0401	CATCTACAGGGTCTCTCTGGG			16-040R	ATGATGTGTGTGTGTCTGAG			16-040E	TGAAATGCTGAGATTAAGTGAATGCTAT		
16-0411	16-0411	GGGTGCGCTCTAATTAATCT			16-041R	AATCTGACATCTCTTATGAACT			16-041E	TCACCTCTGATTAATAGTGAAGCTTT		
16-0431	16-0431	CACACTGAGGCAAGCACTCGGG			16-043R	GCATAGCTGTGTCTATTTAC			16-043E	TATGCTTGGGAGCTGCAATCTGTGACA		
16-0441	16-0441	GCATAATCTTAGCACTTGAAGAC			16-044R	CGATCTGCAAGTCCGCGAGC			16-044E	ACAGCAAACTCATGTATATCAGCACCA		
16-0451	16-0451	TCCGAGGCTCTCTGTGACAGCA			16-045R	CGATCTGCAAGTCCGCGAGC			16-045E	CCAGAGCTGTGTGTAAGAGCTTTCTG		
16-0461	16-0461	TCCGAGGCTCTCTGTGACAGCA			16-046R	ACTCTTTTTAAATTTGAGATGG			16-046E	GGCGCACTCTGGCTCTGCTGCAACTC		
16-0471	16-0471	GGTGAAGGCTCTGAGGCTGAGC			16-047R	AATGATCTATGAGAGAAAGCGC			16-047E	GGCTGAGGCTCTGAGGCTCTCTCATAG		
16-0481	16-0481	AGCTACTGGATGCACTGGTTCGC			16-048R	TGCGCTTCTAGGATCTGGGTA			16-048E	GCTCTGCTCAATCTAATAGTGAAGTAC		
16-0501	16-0501	ATCAATTTGCTGTGTGATGTA			16-050R	CTTGACCAATGATTTGACCTTAC			16-050E	TTAAGACCTTGGCCTTTTCTTCAATTA		
16-0511	16-0511	TGATCTCTCAAGGACTGGC			16-051R	ATCTCTCAACACAGATACGA			16-051E	AACTCACTTAACTAGCTGTGATGTT		
16-0521	16-0521	AACTCTGAGTGGGTTTGGCAT			16-052R	GGTATATTAATGAGGCCCTCTGA			16-052E	CCCTCTCAACTATAGCTGTGTCAATCTC		
16-0531	16-0531	CTCTCCCACTAGGACAGGCAT			16-053R	CAGCTCTCCGATACCCATCATCT			16-053E	ACGTGCTCTCACTAGCACAGCATGCTC		
16-0541	16-0541	CATCTATGCAACAGGTTGTT			16-054R	AACAAGTGTGCTTTCTCTGTT			16-054E	GCTGAGCAATTTGGCTCTCAATAGGACCA		
16-0551	16-0551	CTCTGAGGCTCTGCAAGATGTTTA			16-055R	CAACACATGTGGGTCTAAG			16-055E	GCTGAGCAATTTGGCTCTCAATAGGACCA		
16-0561	16-0561	TGAGAGGCTCTGTGCTTTCTTCC			16-056R	GAATCTCCCAAGGCTCTGAC			16-056E	GAATCTCCCAAGGCTCTGAC		
16-0571	16-0571	CTGGGCTCTCATCTCTCTCTGGC			16-057R	AAGGGGCACTGCTAGAACCGGGCC			16-057E	GTCTCACTCTCCCAAGGCTCTGAC		
16-0581	16-0581	CTTAGCTCTAGAGGTGTGATCTA			16-058R	CAAGTGAACCTCATCTGTATAGAC			16-058E	AATCTGTGTATAGACTCTCAGGCTTTGGCT		
16-0591	16-0591	CTTCTCTGTGTACTAGTCTCTAA			16-059R	AGTGGGCTCTAAAGGTGATCT			16-059E	AGAAGTAGGCAAGCAACCAAGAGCGAC		
16-0601	16-0601	CGGCAAACTCTAAATTTT			16-060R	TCCACAGTCCCGAGGTTTGG			16-060E	CCAGATCACTGAATCTCTGCAAGGCAATC		
16-0611	16-0611	GAGCCAATGCCCAGAAACAGTTA			16-061R	TTCTCATAGGCTAGCAACCCCGCC			16-061E	TCTCATATGCGCATGGCCATGCTCTTCTAT		
16-0621	16-0621	ACTTCTTCTTCTGTCTCTCTCT			16-062R	GAATCCAGCTCTGTGCTGAC			16-062E	GCTGGGCACTCTAGTTTAACCTCGCC		
16-0631	16-0631	ACTTCAAGTCTGGGCTCGGGGC			16-063R	ATCTCGACCCCTGTGAACCCGAT			16-063E	GGAGCAGGCCATCTGTGGGCTGACAC		
16-0641	16-0641	ATAAGTGAATTCCTCAAGT			16-064R	TGTCTCTTCAAGGCACTCTGAG			16-064E	CCCTCTCTCTTGGGCTCTGAGTGAAC		
16-0651	16-0651	TTCTCTGTCTAAATATTTGCGTCT			16-065R	AGGAAACCCCACTCTCCCAAC			16-065E	CTGCTCTCTTGGGCTCTGAGTGAAC		
16-0661	16-0661	GTGACTCTTCCAGAGAGTGCCTA			16-066R	GGAATGGACAAATTTCTACAGATCT			16-066E	CTGCTCTCTCTTCTAGTGGCTGCAATC		
16-0671	16-0671	CCACTCTTCTCTGCTCTCA			16-067R	AGAGAGCTCTGCTTGAATAA			16-067E	GGTGTGAGGCTTTCTGCGCACCCAGAT		
16-0681	16-0681	ACCAAGCTTTTCCCGAGGGCTTA			16-068R	CATTGGGCAAGTATCTTCTG			16-068E	CCGACGGGCTTTCTGCGCACCCAGAT		
16-0691	16-0691	CCATAGCACTGTGCTGGAATA			16-069R	CATTGGGCAAGTATCTTCTG			16-069E	GTCTTGTGCAAGTCTCACTAATTTCA		
16-0701	16-0701	CTCTCAAGCTCTCTGCACTTT			16-070R	CATGGAATACATGCGATAGGAG			16-070E	CTCAGGCTTCTCTCACTCTCCCACTC		
16-0711	16-0711	ACACTCATCTCACTTATATCTTAA			16-071R	TGGAAGAGAGACTGCAAGGACTA			16-071E	GGAATAGGGAAGTCTAGGCTTTGGTGA		
16-0721	16-0721	ACATGTTCTCTCCCACTTA			16-072R	GTGAAAGAGAGACTGCAAGGACTA			16-072E	GAAGAGAGTGTGCAAGAGGCCCAAGTTAG		
16-0731	16-0731	ACATGAGCTGCAAGCAATGACA			16-073R	GTGGAAGCTGAGGACAGCGAGCTTGG			16-073E	GGCCATGCTTCCCAAAATCTCTTATAGACACTG		

SNP	Left Primer			Right Primer			Probe on Slide		
	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	
16-0751	16-0751	TTTAAKGCACCTGAGTTTGGTGA	16-0751	GTGTGCTGTCATACAGAGCTAT	16-0751	TTAAGTTGTTATGCTGTCTCAATGCACTCTG	16-0751	CAGATGCAATTGACAGCAATACCAACTTAA	
16-0761	16-0761	TGACTGCGCTGGGTGTGGATCTCT	16-0761	TTTCTCAGAAATCCATCTCCGT	16-0761	CTGCTTCTCAGACCTCTATCTGTCAACC	16-0761	GGGTGACAGTAGGGTCTGAGAAAGCAGAG	
16-0771	16-0771	CTTGGGGAGAGGTGTATCATGAT	16-0771	TGCAGAGCATTTCCTTACGA	16-0771	ACAGAATTAGATCTGAGCTTCTGCGACG	16-0771	GTCTCCAGAGCTCAGATCTAAGTCTCT	
16-0791	16-0791	TATGAAGATGAAATCAGCAT	16-0791	TTGAGAGCTTTGGATACAGAGGCG	16-0791	AAGATGAAAGTCTCAGTGAAGAGATCA	16-0791	TGATTTCTTCTACTGAAGCACTTCACTCT	
16-0801	16-0801	ATCAAAGCCCATATACCAATCT	16-0801	CTCCCGCAGCAGGAACAGATTC	16-0801	CATCAGCAGTCTCAGTCTGAGTGAAGGCT	16-0801	ACCTCAGTCAAGCAGATGATATCATCTGATG	
16-0811	16-0811	AGCTGTACGACCTGTGATCAAAACG	16-0811	CATTTTACCTCTTGGCAGAC	16-0811	TGTGGAGAGCGCGGAGAGTAGTAGGCA	16-0811	TCCCTCTACTCTCCGCGCTCTCCACA	
16-0821	16-0821	AAATTCAGGCTTTTCAACAACG	16-0821	CTGTGCTTAATGAGAGTCC	16-0821	CAGCTTGTAAATTTGCTGTCTCCGCTGAGCG	16-0821	CGCTCACCGGAGACAGCAAAATACAGCTG	
16-0831	16-0831	AGGAATTCAGAGCTGAAAT	16-0831	GCCAGCTTCCAGGCTGAGATTC	16-0831	TAAGATTGGACAAATTTGCTCTTTCTTAG	16-0831	CTAAGAAAGAGCAAGATTTGTCCAACTTAA	
16-0861	16-0861	TTGAGCTTGGGGGTGCTCCCTCGC	16-0861	ACCTCGACAGACATCTTGG	16-0861	GAGTGTGAGCTCTGAGCTGTGCCACGC	16-0861	GCCTGGGACAGTCTCAGGCTGCACCTC	
16-0871	16-0871	GCAAGGGAAGATGTATCAAT	16-0871	CAGGTGTGTTGGTTAAGCAT	16-0871	CATGGGGTGAAGGGGACAGGCGCTCC	16-0871	CGAGGCTGTCTCCCTTTTCAACCCCATG	
16-0881	16-0881	AGTCGAGGATGTAGGTGATGAC	16-0881	TTTGGAGTGTGCTGCTACTGTGG	16-0881	GACCTCTCTGGGGGAGCTCTGGGTGG	16-0881	CCACCGCAGCTCTCCCGCAGGAGGCTC	
16-0891	16-0891	CATGACATGAGTGAAGGCGC	16-0891	TTTGGAGCTGACTCCCAAGATGG	16-0891	AGCTTACGCTTCTTCTGCCCACTAGCAT	16-0891	ATGCTAGTTTGTGGGGAAGAAAGCTAGAGCT	
16-0901	16-0901	GGATGGGGAGGTGGGCCCTTA	16-0901	TCAGGCTGACAGAGGACATC	16-0901	GGACACTCAGGCACCTTGTGACCTCTAC	16-0901	GTGAGGCTGCAACTCAAGTGCCTGAGTGTCC	
16-0911	16-0911	TTTGGGCGAGCAACCTGGC	16-0911	GATTAGACTCTACAGCAACTGTA	16-0911	ACAACTGTAAAGTCTGCGATGACAAACA	16-0911	TGCTTTTCTTCTCAGCAGACTTTTACAGTTCT	
16-0921	16-0921	GTTCATGTGTCAATTAACCTGTTAC	16-0921	GCMAATTTGACTAGGCAACTT	16-0921	TTATTGGCGGTTGGGACTATTATCTA	16-0921	TAGATTAATATGTCCTCCACCGGCAATA	
16-0931	16-0931	CTACAACCTCAATTCAAGT	16-0931	CCCTTTTCAGAGCAGCTTA	16-0931	CAGCCTTATTCAAATACTGATGATGCA	16-0931	TGCACATCCATCAGTTATTGTAATAGGCTG	
16-0941	16-0941	ATCCAGAAATATAGACAGGCTCTTA	16-0941	AGTTATTTTTCACACCAAACT	16-0941	TTGCTGTGACTTTCCATCTGAGAGGGA	16-0941	TCCCTCTCAGAAATGGAAGATCAGACGAA	
16-0951	16-0951	AAGGGAAGGAAGACATATGG	16-0951	GTCTGTGCTCTGATTAAGT	16-0951	AAGTTTACACTCTCACTTAACTAGAGGA	16-0951	TCCCTCAGTTAAGTGTGAGATGTAACTT	
16-0961	16-0961	TGCTTTCAGCTGGGCTCAG	16-0961	TCAGCAGGCTCAGAGATGGGG	16-0961	GGCTCAGGTGACTCAAGGGGAAGCACT	16-0961	AGGTGCTTCTCCCTTCTGAGTCACTCGACC	
16-0971	16-0971	AAGTTGTAGATGGCAGCTGGTA	16-0971	TGCTCTGCTCTCTCTTGG	16-0971	TTCTCAAAATGATTTCCCATCTCCACACA	16-0971	TGCTGGGATGGGAAATTCATTTTGTAGAA	
16-0981	16-0981	AGATGTGTGCTCATATACACCTG	16-0981	CAGTGTGTTTGGAAATTA	16-0981	GGAAAGTTAGAAAGATGTCTGATGAG	16-0981	CACCTACGATGACATGCTTCTTCACTTTC	
16-0991	16-0991	GGAGAAAGAAAGAAAGAACTCAAT	16-0991	GACATGTGCTGGCAGAAAT	16-0991	TGGCTCTCTCTCGAAGTTTCCAAATGCTCT	16-0991	AGGCAATTTGGAACTTCCAAAGAGGCA	
16-1001	16-1001	ATTAGGATTCCTTGTCTTCTGG	16-1001	CATGGGCTCTCTGTTTCAAGT	16-1001	TGGCAGCTTGGGCGACGAGCAAAATGC	16-1001	GCATTTCTGCTGCCACAGCTTGCCA	
16-1011	16-1011	CACAGATTTTGTCTTGTCTGG	16-1011	ATTAGTACAGCATTTGTGTATGTA	16-1011	CTATTTACTGAGCATCTACTGTATGCTGA	16-1011	TCAGGCAATACAGTATGCTCAATTAATAG	
16-1021	16-1021	GCTGTGCTGCCAGGCCACG	16-1021	TGCAACCTGTGAGGCAACA	16-1021	CACAGGCTGTGCTCCCACTCTTATTC	16-1021	TGCGTGGTGGCAGCAGGCGCTGTG	
16-1031	16-1031	CACCTCTGGAATTAATGTGAC	16-1031	TTTACAGCAGAGGCAAGATATG	16-1031	GTGATGCTTCTTCTCAGATGTGAAATA	16-1031	TATTTTACATCTGACAAAGAACTGAC	
16-1041	16-1041	CACCTGCTCTCATCTTTTAC	16-1041	TAGCTTTCACAAACATTTTCTTTA	16-1041	GTGAGGCTGCAAGGTATGATTTGCTACCC	16-1041	GGGTAGCAAACTAATACCCTGCACCTACC	
16-1051	16-1051	ATGAAGCTGGGTGGTCTTTGGTGA	16-1051	ATCAAGGCTCTTAAAGAACT	16-1051	GTGATGCTTTTGTGAGATGTGAAATA	16-1051	GCATCTGCTCTCTCTGCTGTGTAACAGG	
16-1061	16-1061	TCTCTGGGAAAGAGGAAAGCTAA	16-1061	CTCTCTGGGAGATATGCTCTGTTA	16-1061	CTCTGAGTGTAACTCAAGTTGGCCATGC	16-1061	GCATGGCCCACTTGATGTTACACATAGGT	
16-1071	16-1071	TGTGGGCGACTGGAAATCGG	16-1071	CCGCGCCACGCTGACATCAGTA	16-1071	TGCTGAGAAGGCCAGGAAGCTTGTCTG	16-1071	CAGACCAAGCTTCTCTGGGCTTCTCACA	
16-1081	16-1081	GCCTCAATGACGACATCAGCG	16-1081	GGCAGGCTAGGTGAGCTGGTGA	16-1081	TAACAGAGGCACTGGGAGAGGTGACTTA	16-1081	TAGATGCTAGCTCTCTCTGGGCTTCTGTTA	
16-1091	16-1091	ACTGTGCTGGCTCTCATGTGA	16-1091	GCACACCGGAGAGCTCTCTCTTA	16-1091	GCACGAGGCAACTAGGCTGTGCTCTT	16-1091	TAGGAGCAGCAGCTCAAGTTTCTGCTGCTG	
16-1101	16-1101	GACCTTATGTAATGTGACGCG	16-1101	CTCTCTGTAAATGTTAACTCGAT	16-1101	CTATGTAAAGCTGAGGCCATTTTGTCCCA	16-1101	TGGGCAAAATGGGCTCAGTTCTTACATAG	
16-1111	16-1111	CTACTGGGTTACATTTGAGACCG	16-1111	GGGAGCAATGTAATGTTGTTA	16-1111	GATTTCAAGGCAAGTGTGCAATGCGCTG	16-1111	CATGGCATGGAATCTGTGCTGCTCTTTC	
16-1121	16-1121	TCATATGGTATGGCATGCACT	16-1121	GAAAGCAGCAGCAGAGAAA	16-1121	ATTTCAAGGCAAGCTGCAACAGGGAAT	16-1121	ATCTCTTGTCTCAGGTGTCTGTGAACTG	
16-1131	16-1131	TTTACATCTCTACCTGTTCACAC	16-1131	TGAATGTAATGGGAGCTTA	16-1131	ACAGTGAAGTTTCTCAATGTCTCCCTATTA	16-1131	TAATAGGGGACAAATGAGAAACTCAACTGT	
16-1141	16-1141	GTCTCTCTGATGACCAATAATG	16-1141	TTCTCTGATCAGCTGCTGCTT	16-1141	ACAGTGTGATTTCTCAATGTCTCCCTATTA	16-1141	TAATAGGGGACAAATGAGAAACTCAACTGT	
16-1151	16-1151	TGAAAGTCTTCTCTGGGTGCTCA	16-1151	AAGACTGAGTCTAGATTTCTGCTGG	16-1151	AAGACTGAGTCTAGATTTCTGCTGG	16-1151	TAATAGGGGACAAATGAGAAACTCAACTGT	
16-1161	16-1161	ACCAGTGGCTGCTGCTGCTTA	16-1161	TTATCTGTGCCAGATGGGACAC	16-1161	CAGGTTACATATTAAGTCTTGTATGACCTC	16-1161	GGAGTCTACAAAGAGATGAAATGAACTG	
16-1171	16-1171	CAGCTAGACACCAATACCTGGCTCA	16-1171	TATCTGTGCCAGATCATCTT	16-1171	CTGTCTGGCCTTCAAGTTTCACTCAGCAGA	16-1171	TCTGCTGATGAAACTTGAAGGCAAGACAG	
16-1181	16-1181	ATCGGCGTCTGAGCGGCTGA	16-1181	TCTATTTCTCTTCAAAATGTGAC	16-1181	GACCAATGCAACAGCATATTTGGGATG	16-1181	CTTGTGTCAAGATATGTCTTGGCTATGGTTC	
16-1191	16-1191	GAAAGATTTTCTCTCTCTCTCTCT	16-1191	TGTGAACTGCTGCTACTATAGACT	16-1191	CTCTGCTGACCACTCCCAAAAAGGC	16-1191	GCCTTTTGGGGAGGCTGTCTCAGCGAAG	
16-1201	16-1201	AAAGGAGAAATACAGATCTTCCCTC	16-1201	CATCAGATGCTGCTACTGCTCTCGC	16-1201	TTCGCAATTAAGATCCCTCTCTCTCT	16-1201	AGAGAGAGAGGGAATCTTAATGATGTTCA	
16-1211	16-1211	CAGTAAATCCAGGCGAGATGTATG	16-1211	TGGGAATATGCTGCTGGA	16-1211	TCTCTATCCGAGGCTCAGAGGAAGATTATA	16-1211	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1221	16-1221	TAGACAAAGGATGATGACTTGG	16-1221	CTCTTTGCTGCTGCTGCT	16-1221	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1221	TAGATGACAAATTCCTGACAAACAACTGGAT	
16-1231	16-1231	GCTGGAATTAACATGTGATGAACT	16-1231	ACATTTATGAGCACTGCTTGGAACT	16-1231	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1231	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1241	16-1241	CTCAAGTGCATGCAATGAAACCTTA	16-1241	GGGCGCTGGGAGCAAAATTCGTC	16-1241	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1241	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1251	16-1251	ATACCATAGCCACCCGACAC	16-1251	GGGCGCTGGGAGCAAAATTCGTC	16-1251	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1251	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1261	16-1261	CTACTGAATCAGAAACTCTGCG	16-1261	GGGCGCTGGGAGCAAAATTCGTC	16-1261	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1261	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1271	16-1271	GTCTGATCATCAGAAACTCTGCG	16-1271	GGGCGCTGGGAGCAAAATTCGTC	16-1271	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1271	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1281	16-1281	TGCTATCATGTAGTACGATGCTG	16-1281	GGGCGCTGGGAGCAAAATTCGTC	16-1281	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1281	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1291	16-1291	CCGGGCAATTTTCAATGCGCTTA	16-1291	GGGCGCTGGGAGCAAAATTCGTC	16-1291	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1291	TACTATCTCTCTGACGCTGGGATGAAAGA	
16-1301	16-1301	CCGGGCAATTTTCAATGCGCTTA	16-1301	GGGCGCTGGGAGCAAAATTCGTC	16-1301	TTCTCATCCGAGGCTCAGAGGAAGATTATA	16-1301	TACTATCTCTCTGACGCTGGGATGAAAGA	

Left Primer		Right Primer		Labeled Probe		Probe on Slide		
SNP	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')
16-1311	16-1311	GCTTGGATTATCTGTGTTCAT	16-131R	GGCTGTGCTGAACTCCCAAC	16-131E	TCTGAAGCTTTTGAAGAATACCTGAGGAG	16-131A	CCTCTCAGGTATTCTTAAAGGCTTCAGA
16-1321	16-1321	TTCTCAGATTCTGTGGATCT	16-132R	TTCCCTGGAGGAGATTTGAC	16-132E	TGCTCATCAATGGAAATGAGGTGACAG	16-132A	GCTCAAGCCCTTCATCTTAAATGGCCAC
16-1331	16-1331	AGCCAGAGTGATTTCTAGATAT	16-133R	ACAATCTGTGTGTTTGAAT	16-133E	TAGCTATGGAATGGGACAGGCTTGTAT	16-133A	TTCAAGACCTTCGCACTCTTATGAGACTA
16-1341	16-1341	TGGCTGGCTGAAATATATCT	16-134R	TTGGCTTTCACAAGGTGGGCG	16-134E	GGCCGACTGTC GAGCACTTCTTTGGAA	16-134A	TTCCAAAGGAAGTGCTGTAACAGAGCTGCGCC
16-1361	16-1361	ACTTGTTCATATGGAGAGTAT	16-136R	TTACAGACAGGGGGTGCTGGGA	16-136E	CTTACAGACAGGGGGTGCTGATATGTA	16-136A	TCATATATGACAGATCTGTAACAGAGCTG
16-1381	16-1381	GGATTCCTATGTCTCACTCCG	16-138R	AGGAGGTCAAGCTGATCTTC	16-138E	CATCTCTTCTGAAGACCCAGCAATCCC	16-138A	GGATTGCGCTGGGGTGCTTCCAAAGATG
16-1391	16-1391	CAGCTTGATGAAGAAATTCG	16-139R	ACCAGAGCTAGCTCTACAT	16-139E	TGGGATTGTGCGCCCTGGTAAGCTGGAAG	16-139A	CTTCTCAAGCTTACAGGGGCAAAATCCCA
16-1401	16-1401	GAGACCACCTCTCTGCAGCTCA	16-140R	TTCTGGCGCCACCAAGGGGAAAC	16-140E	CAGCTCAGGATGTTGTATGTAAGGATGTC	16-140A	GACATCTCTGAACTACAAACATCTCTGACTG
16-1411	16-1411	GCTGACATCTGCTTCTCCCGGCA	16-141R	TGGGAAACCAAGGGGCTTGGCATAG	16-141E	TGGCATAGCTCTGTTTGAAGATGAGCTTG	16-141A	CAAGCTCATGCTTAAACAGAGGACTATGCCA
16-1421	16-1421	GGGTGGCCAGGCTCTGGGTA	16-142R	GAAAGCCGCTGCTCTCTGTGTGTC	16-142E	GGCTTAGGGGAGGCTCTACAGAGCCCA	16-142A	TGGGCTGCTGAGGCTGCGCCTTAGGC
16-1431	16-1431	CATCATCAGGGGACAAGTCCCTCTG	16-143R	GAGGTAGACAGCTCTCGGTGTC	16-143E	GGCACCATTCTCTTGAAGAGACCCAGGA	16-143A	TTCTGGCTTCTTAGGAATGATGTGTGGC
16-1441	16-1441	AGAGCCAGCTGTGCCAGAGCTA	16-144R	GGGTAGACAGCTCTCGGTGTC	16-144E	TGGATGGGATTCAGCTATCTTCCCTGTTA	16-144A	TAAAGAGAAATAGGAGTAAATCCCCACAC
16-1461	16-1461	GGTTGGCCCAAGGTTTAGGAG	16-146R	AGAGGCTGGGAGAGGGGGCTTA	16-146E	CTGGCTGGTTTGTAGTACCGGTAAGACTTTC	16-146A	GAAAAGGTTACCCGGTACTAAACAGCCAG
16-1471	16-1471	GAAAGAGTACAAATCTCTCGGG	16-147R	ATTCTATCTATCCCAACAACAT	16-147E	TGATATACCTCTGATTAATGATGCTGTCG	16-147A	CAACCATCTCTTATAGGGGAGTATCTCTCA
16-1481	16-1481	AAATTTGGTTGGATCTGCTGGTA	16-148R	CTTGACACCTTCTGATTAATGCTGTCG	16-148E	GTATCGATACCTCTGATTAATGCTGTCG	16-148A	CAGCAGATCAATCAGAGGATTAQATTAAC
16-1491	16-1491	TCAGAGACAAGCTGAGGAATA	16-149R	CACCTAGATAGCACTTCACTAA	16-149E	TCAGTTTTCAGCAAAATGTTAGAGAGGAG	16-149A	CTCTCTCTAGACATTTGCTGAACAATGA
16-1501	16-1501	AGCCAGACTGAACCACTGTATA	16-150R	GACCTGAGGAATATACCTGTAT	16-150E	CTGTAAATTCGTCTAAACATCAGGTAGG	16-150A	CTCTCACTGATATGTTTGACGAATTAACG
16-1511	16-1511	TTCCCGCACTCTCTTGATC	16-151R	TGAACAGGGCAAGAGCAACCG	16-151E	GAGTATGCTCTCAAAGCAAGGCTAGAAAT	16-151A	ATTCTACGCTCTGCTTTTAGGGTATTCTTC
16-1521	16-1521	TGGGCTAGCCCTGGGGAGAAATG	16-152R	CAGGCCAGACTCGATCCCTCTATC	16-152E	CAGACCCAGGCTAAGCCAGGGGGA	16-152A	TCGCCCTGCTTATACCGCTGGGTCTG
16-1531	16-1531	CTGCGCTATGCTCTTCAACGGC	16-153R	CAGGCTGGGAGAGCTTGGC	16-153E	CGCGCATCTCTAGCAAGATGTGAAAGGC	16-153A	TGCTTCCATCTTCTGCTTAGGAATGCGCG
16-1541	16-1541	TTCTCAACCTCTAGCTCTCGGGG	16-154R	CTGCCAGCTTGGCTTTCTCAT	16-154E	TGGAATCTGTTTAGCACTAGGTGTGACAA	16-154A	TTGTCAAGCTGCTCTCAAGGATGTGTTCA
16-1561	16-1561	CAGAGCTATTAGCAGGAGCTCAT	16-156R	AQAAGCTGGAGCGGTCACTCG	16-156E	AGCCAAGCCGAGTGGCCGTTGATGC	16-156A	GCATCAGGGCAAGCTCGCTTGGCT
16-1571	16-1571	CTTCAACCTAGGGTCTCTATGG	16-157R	CTCCGTGTAGTCAACCCCACTC	16-157E	TGCACCTCAAGATCATGCTCTTTTAACC	16-157A	GGTTAAAGGAAGGACATGATCTAGGTGGGA
16-1581	16-1581	CTTAACCTGTCTCCCTTGGCTTCA	16-158R	ACCATCTGGCAGACAGCTTC	16-158E	TGGAACATGGAATGGGAATGTCGAG	16-158A	CTCTGCAATGCCATGCGCATGTTCCA
16-1591	16-1591	TGGCTCTAGAAATATCTCA	16-159R	CATTCTCTGTGACCTGTC	16-159E	TGGTGAATAAAGATAAACAGCTGTCTCA	16-159A	TGAGACACTGTTATCTTTTATTCTACCCA
16-1601	16-1601	CTGTGCTATTTGTGTGCATAA	16-160R	CTCTGGGCAACCAACAGTTA	16-160E	ATTGATCTGCGAGCAAGTCTCTCTTC	16-160A	GAAAGCAAGCACTGCTCTAGCTGAATTAAT
16-1611	16-1611	AAGCCTTCAGGGTGAGGACAGAC	16-161R	GGGCACTCCCGGCACTAATAG	16-161E	TGGAATCTAGGGGGCTGGGATGGA	16-161A	CTCTTCCAGGCCAGCCTTCTCTCCAG
16-1621	16-1621	CAGAAAGAGCGGGGGAGCTGGC	16-162R	AGCAAGAGTGCCAGCTGGC	16-162E	CTGGGAGAGAGGGCTGGGCTCAAAGG	16-162A	CCTTTGAGCCAGCCTTCTCTCCAG
16-1631	16-1631	TGCTCTCTCTCTATAGAGAGTTAT	16-163R	CCCTCTGTCTCACTGTAGGTGCTTA	16-163E	AGCAATATGAATATCAGAGGCTCACAGA	16-163A	CTCTGCAAGCACTCTGATATTAATGTCT
16-1651	16-1651	TGATATTTGACACACTTTCG	16-165R	TGATGACTCATGTAAACCGGA	16-165E	GCCAGGTATGCGCGTACGCTGTTCCAC	16-165A	GGTGAAGACCACTAGCCATACCTGCGC
16-1661	16-1661	CTGAGCGGATATAGAGCAAGGGGCA	16-166R	GTGATCGGCTGTCAAGCGGGT	16-166E	GGCAGGTGTCACTGCTCTTGTCTG	16-166A	TGTTGGAAGGAAATTTCTCATGACACCTGCG
16-1671	16-1671	GCCTCTCTGGCCCTCTGCCTA	16-167R	CCCAAGATATGGGCCACACAGACGCC	16-167E	CTGATGAGGATATGAGAGGCTGTGTCAC	16-167A	GTGTGCGGCTGCTCTTGGAGGAAGCAG
16-1681	16-1681	GCTCACCGACCTCTGTGAGTA	16-168R	TTGTTTCAACACCCATGTCAATA	16-168E	GGCATGCTTCCAAAGAGGTCCAGACACC	16-168A	CTTGGGCTCTTCAGTGAACCCATGCC
16-1691	16-1691	TGTGAGAGCTGTGTGAGCAACAG	16-169R	TTGATGTCCCATACCAAGCGGCA	16-169E	GGCATGAGTCACTGGAAGGCCACAG	16-169A	CCGACACTCTGGBAAATGTTCTGTGAGC
16-1701	16-1701	ATGGTTATGTCAAAACCGGA	16-170R	AATGGTTTAAAGGGTTCCCTCTA	16-170E	TTTGAGTGATATGTAATCTCTCTTGTCTGG	16-170A	CCGACAAGGAGAGATTACATCTCAACTCAA
16-1741	16-1741	GGGCGCTTTCTTAGGAGAGTTGAC	16-174R	AGATCCGACCTGTAGAAATCAAT	16-174E	TTTGAGTGATATGTAATCTCTCTTGTCTGG	16-174A	CCAGCAAGGAGATGTTACATCTCAACTCAA
16-1751	16-1751	TTCGCGCTCAGCAGCAGGCG	16-175R	ACTCATTTTAAGTGAAGCTCAAT	16-175E	CTGAGGCGTGTTCAGTTTCTGTGTA	16-175A	TACAGAGAAATCGAAACACCGCTCAGG
16-1761	16-1761	CGCTCTCAGTGAAGGTTGGGT	16-176R	TTAGGAGCTCCGCTTCCGCTG	16-176E	GAGCTCGAGCCCTCTCTGAGCAGCCTC	16-176A	CTGCGAGCGCTCTCTGAGCAGCCTC
16-1771	16-1771	GTATTAATATGATCATGAGTCTGAC	16-177R	TTTATAGGCGCTCTCGGGTCAATG	16-177E	ACAAGAACCTTAAACACCAAGCCTGTGTTTG	16-177A	CAAAACCAAGCTGTGTTTAGGTTCTGT
16-1781	16-1781	CAATATAGAAAGCGGGGCAAT	16-178R	CTCAGCTGGCCTTTTGCTC	16-178E	ATGGGTAAATCAGTCTCACGCTCATAGGC	16-178A	GAAATGCAATATAGGCTGATTAATACCAAT
16-1791	16-1791	TGAACATACGCTGCAGGCAAC	16-179R	AGGAAGTATACGAGGTGTGTTA	16-179E	GGGCTCTGGAGCCCTAAATGATGTCGACTTC	16-179A	GAATGCAATATAGGCGTCTCAGAGGCC
16-1801	16-1801	CCCATAGACATGAGAGGCGCTT	16-180R	GGAGTGACCGGAGCTACATGCG	16-180E	CAGCTTGGCAGGCTGGCGGCTCT	16-180A	AGGCGGCCACCTCTGCCAAGCTG
16-1811	16-1811	AAGTAAAGATACCGCAGAGCA	16-181R	GGAATGTGATCACTGGAGCTCTA	16-181E	TCACGAGGAGCAGGGCAGGCTCT	16-181A	GGGCGCTGCTCTCTCTCTCTCCGTA
16-1821	16-1821	TTTCTTGAGGATGTCTCAACG	16-182R	ATTGGCTCTGCGCGGAGCG	16-182E	ACACGACAGACGCCCAACCCGAAG	16-182A	CTTCTGGGTGGGCGTCTCTGCTGT
20-0011	20-0011	TAGACACTTACTATGTGCGCTC	20-001R	TTTCTCTATTGGGCAACGGG	20-001E	AGTGCCTATGTCAAGATGGAATGAGGA	20-001A	TCCTCTACCTCAATCTGTGACATGAGCACT
20-0031	20-0031	AGCACTTCTGGAAAGCAAGCG	20-003R	CACAGTTACAAACAGCAATTTATC	20-003E	TTCAATGCGTGAATATATGAGACAGCG	20-003A	CCTGTGCTTCCATTAATCTACTGACCTATGAA
20-0051	20-0051	GATTCTCTCTGGACACGGCTTAT	20-005R	CCAGGAAAGTGGTGTGTTCTTATC	20-005E	CACAGTGAACCTTATATGTCGGCTCACTGT	20-005A	TAGGAGCGGCACATAAGGCTCTCACTGTG
20-0071	20-0071	GAATACATCATCTTCTGTTGAT	20-007R	TGACACTATGGAATGGAATTAACATTC	20-007E	AGCCAGATTCCTCTCTTCTAGCATCCCA	20-007A	TGGGATGCTGAAGAGAGGAATCTGGCT
20-0081	20-0081	CAGGTGGAATGGAGGCTGTCTCAT	20-008R	TGTGCTCAAAATCCCAACAC	20-008E	ACCTGTGTGATAGGAGCAATTTTCCCA	20-008A	TTGGGAAACATGGTCTCTATACAAACGCT
20-0101	20-0101	ACAAGACTGCAACTTACATCTGTA	20-010R	AGGGTAGACAGCAAAACCGT	20-010E	GTTCACTCAACAGTATATGTATGCTAGGCA	20-010A	TCCTACCATACAATAAAGCTTGTAGTGAAC
20-0111	20-0111	GCAAGTTGGCATGTATATCTCG	20-011R	TAAAGCAATCTCTTATTTAGGTTC	20-011E	TTTTCTGTGACCATGATATGATGTATCT	20-011A	AGATAGCAATCTTACTACTACCAAGAGAA
20-0121	20-0121	TGTTTCCATGAACTATTTA	20-012R	GATCTGGACATCAAAACCTTGC	20-012E	TTTTCTGTGATGATATCAACACAGCAC	20-012A	AGATAGCAATCTTACTACTACCAAGAGAA
20-0131	20-0131	CTTGGGAGAGGGGCAAGCTAA	20-013R	TATCCAGACTCTTGGAACCTTGGT	20-013E	TTTCAATTAACAAGACTTGGGCAACTGGT	20-013A	ACCAGTTGCCCAAGTCTTGATAAATGAAA

Table II

SNP	Name	Sequence (from 5' to 3')	Left Primer	Name	Sequence (from 5' to 3')	Right Primer	Name	Sequence (from 5' to 3')	Right Primer
20-0141	20-0141L	TGCACACAGTATACCTTCT	20-0141R	AGTACTGCTGCTGGGACACGG	20-0141E	GGTCTCTAGCATTAAGTGTCTCCCTGG	20-0141A	CGAGGGACACCTAATCTCTACGGAACC	
20-0151	20-0151L	TCATCGAGTGTCTATGACAT	20-0151R	AAGATCAGAACAGCTCTCAT	20-0151E	ATGATCAGACACGAAATTAACATAGCC	20-0151A	GCCTATGTTAATTTCTCTGCTGTATCAT	
20-0171	20-0171L	CCCTACCTGTGCTCTCTCTGCA	20-0171R	TGTTCTGCGGCACATTTTAT	20-0171E	TTATCTCAGGCGAGTGGCCCAAGATAGG	20-0171A	CCATCTGCGCCACCTGCTCTGTGATAA	
20-0191	20-0191L	AAATAGAGTAAAGCTCTTGACCTGG	20-0191R	TATCAGACGCGTGAATGACATA	20-0191E	TATCCTTCATAGTATTAATGATTTATGAG	20-0191A	CTACATATAATGCAATTAATGAAAGGTAT	
20-0211	20-0211L	GAATAGAACTAGCAGAGATGTA	20-0211R	AGCCACCTGCAAAACATCTTC	20-0211E	GAGGCAATATCTGACTACAGCCCTAAGGA	20-0211A	GTGACCTTTAAAGAGAGACATCATTCACG	
20-0231	20-0231L	GAATACCACTGCTATAGAAACG	20-0231R	TGTTAGTGTGTCTTAATGG	20-0231E	CTGTAATGATGCTCTCTTTTAAAGGTCTC	20-0231A	GTGACCTTCCACAGGTTTCACTGGGAGCCA	
20-0251	20-0251L	GGGGGTTAGGAATGTCAATAAAG	20-0251R	CACCTGCTAGCTCTTGCTCT	20-0251E	TGGCTCCACCTGAAACCTGCGCATGCTAC	20-0251A	ATGCTATTCCTCTCTCTGCTCTTCAAA	
20-0261	20-0261L	CAGAGGATTGGAACAATATG	20-0261R	AGCCTGCTAGCTGACCTCTCTA	20-0261E	TTGAAATCCGAGCAAAATGGAATAGCAT	20-0261A	CTCTGTTTAAAGCCACAGAAAGAGACGAG	
20-0281	20-0281L	TAAAGCATTTCTGCTGCT	20-0281R	ATCAGATTGGAAGATTCTCTAAT	20-0281E	CTGCTCTCTCTCTCTGCTGCTTAAACAGAG	20-0281A	CTCTGTTTAAAGCCACAGAAAGAGACGAG	
20-0291	20-0291L	AGGAGGAGGATATGGGAAAAA	20-0291R	TGAACCCAGCAAAATGGCTTCA	20-0291E	ACTTTTGCTCTGTCGCCAGCAAAATGACTT	20-0291A	AGTCTATGCTCTGTCGCCAGCAAAAGGT	
20-0301	20-0301L	TTTGAATCCCAAGATAAAAA	20-0301R	TATACCTTTGCTCTCATGATGTGAT	20-0301E	TGCCATCTGCTGCTTACTCTACTTTGATG	20-0301A	GAAGAAATGTAATGAGAAATATTAATCAAAAT	
20-0311	20-0311L	AGAGGGTTTGAAGAAAGTTGCAAT	20-0311R	TGCTACATGACAGACACTCAAT	20-0311E	CTTTGTGATTAATAATTTCTGACTTCTCTC	20-0311A	TTACTTATCTAGTCTCTAGGACAAGAG	
20-0321	20-0321L	CATTACGTTGCTGCAATCT	20-0321R	TTCTCTCAAAACCTCTCTCTT	20-0321E	CTTGTGCTGCTCCACATTCATACAGGCTAG	20-0321A	CTAGCTCTGTAATGATGTGGAGCCACCAAG	
20-0331	20-0331L	CATTACACATTTGGGTGCTGCTG	20-0331R	TATCTCAACACCTCTCTGCTTGA	20-0331E	CAATATTAAGATACAGACATAAAGGGGAG	20-0331A	CTCCCTCTTTATCTCTGATTTCTATATG	
20-0341	20-0341L	AGCCTTGTCTAAGTGTCTAGACT	20-0341R	AGTCGAGGTGGTACGAGGTAG	20-0341E	CATGGCAAACTCTTATGATGACAGCTATCA	20-0341A	GTATGCGAGGAGGAGGTGCTTACAGGACTG	
20-0351	20-0351L	GAATATTCAAATGCTCTTTGTA	20-0351R	AAGGAACCTGCTGTCTGGAATA	20-0351E	CAATCTGTAAAGCTCTCTCTGCGATAC	20-0351A	CTAGATAATTCACACATGCTCTCTGTT	
20-0361	20-0361L	ACAAAGCCACAGGTGCAAGGATG	20-0361R	TGTTTATATCAGTCTCTCAACAA	20-0361E	AAACAATGAGAGTAATAGCATCTATCG	20-0361A	CGATAGATGCTATTTCTCTTTAGGAATA	
20-0371	20-0371L	TGCGGCTGATTCACAAAC	20-0371R	CACTGTAGCTAGTTTCTCTGAT	20-0371E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0371A	TGCTGCTGCTGCGAGGCACTTCTATGAAA	
20-0381	20-0381L	GAGACTGTTACAGCCCTGTAG	20-0381R	TCCTCAGGCTGATCCAGACCTAGT	20-0381E	GGCTCAATGTTTCTCCCTCTCTGTA	20-0381A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0391	20-0391L	GGTGGATTTCTCAATTC	20-0391R	AGAGTCTATCTGCTTCTAGCG	20-0391E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0391A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0401	20-0401L	GAATCTAACTCTCTCTACAGCG	20-0401R	CACTGTAGCTAGTTTCTCTGAT	20-0401E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0401A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0411	20-0411L	CTTAGACAGATATGCTCTAAT	20-0411R	TAACCTTTGCGACTTATGCGAC	20-0411E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0411A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0421	20-0421L	CAGATGGGACAAAGATTAAC	20-0421R	CAATGCGCATATGATGCTGA	20-0421E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0421A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0431	20-0431L	GCATCTCTCCACATGTGTGTA	20-0431R	TAACCTTTGCGACTTATGCGAC	20-0431E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0431A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0441	20-0441L	GATAGTGTGACAGATCTATTTGCTA	20-0441R	CAATGCGCATATGATGCTGA	20-0441E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0441A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0451	20-0451L	GCATCTCTCCACATGTGTGTA	20-0451R	TAACCTTTGCGACTTATGCGAC	20-0451E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0451A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0461	20-0461L	GATAGTGTGACAGATCTATTTGCTA	20-0461R	CAATGCGCATATGATGCTGA	20-0461E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0461A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0471	20-0471L	GCATCTCTCCACATGTGTGTA	20-0471R	TAACCTTTGCGACTTATGCGAC	20-0471E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0471A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0481	20-0481L	GATAGTGTGACAGATCTATTTGCTA	20-0481R	CAATGCGCATATGATGCTGA	20-0481E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0481A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0491	20-0491L	GCATCTCTCCACATGTGTGTA	20-0491R	TAACCTTTGCGACTTATGCGAC	20-0491E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0491A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0501	20-0501L	GATAGTGTGACAGATCTATTTGCTA	20-0501R	CAATGCGCATATGATGCTGA	20-0501E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0501A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0511	20-0511L	GCATCTCTCCACATGTGTGTA	20-0511R	TAACCTTTGCGACTTATGCGAC	20-0511E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0511A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0521	20-0521L	GATAGTGTGACAGATCTATTTGCTA	20-0521R	CAATGCGCATATGATGCTGA	20-0521E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0521A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0531	20-0531L	GCATCTCTCCACATGTGTGTA	20-0531R	TAACCTTTGCGACTTATGCGAC	20-0531E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0531A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0541	20-0541L	GATAGTGTGACAGATCTATTTGCTA	20-0541R	CAATGCGCATATGATGCTGA	20-0541E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0541A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0551	20-0551L	GCATCTCTCCACATGTGTGTA	20-0551R	TAACCTTTGCGACTTATGCGAC	20-0551E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0551A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0561	20-0561L	GATAGTGTGACAGATCTATTTGCTA	20-0561R	CAATGCGCATATGATGCTGA	20-0561E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0561A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0571	20-0571L	GCATCTCTCCACATGTGTGTA	20-0571R	TAACCTTTGCGACTTATGCGAC	20-0571E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0571A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0581	20-0581L	GATAGTGTGACAGATCTATTTGCTA	20-0581R	CAATGCGCATATGATGCTGA	20-0581E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0581A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0591	20-0591L	GCATCTCTCCACATGTGTGTA	20-0591R	TAACCTTTGCGACTTATGCGAC	20-0591E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0591A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0601	20-0601L	GATAGTGTGACAGATCTATTTGCTA	20-0601R	CAATGCGCATATGATGCTGA	20-0601E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0601A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0611	20-0611L	GCATCTCTCCACATGTGTGTA	20-0611R	TAACCTTTGCGACTTATGCGAC	20-0611E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0611A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0621	20-0621L	GATAGTGTGACAGATCTATTTGCTA	20-0621R	CAATGCGCATATGATGCTGA	20-0621E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0621A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0631	20-0631L	GCATCTCTCCACATGTGTGTA	20-0631R	TAACCTTTGCGACTTATGCGAC	20-0631E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0631A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0641	20-0641L	GATAGTGTGACAGATCTATTTGCTA	20-0641R	CAATGCGCATATGATGCTGA	20-0641E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0641A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0651	20-0651L	GCATCTCTCCACATGTGTGTA	20-0651R	TAACCTTTGCGACTTATGCGAC	20-0651E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0651A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0661	20-0661L	GATAGTGTGACAGATCTATTTGCTA	20-0661R	CAATGCGCATATGATGCTGA	20-0661E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0661A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0671	20-0671L	GCATCTCTCCACATGTGTGTA	20-0671R	TAACCTTTGCGACTTATGCGAC	20-0671E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0671A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0681	20-0681L	GATAGTGTGACAGATCTATTTGCTA	20-0681R	CAATGCGCATATGATGCTGA	20-0681E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0681A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0691	20-0691L	GCATCTCTCCACATGTGTGTA	20-0691R	TAACCTTTGCGACTTATGCGAC	20-0691E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0691A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0701	20-0701L	GATAGTGTGACAGATCTATTTGCTA	20-0701R	CAATGCGCATATGATGCTGA	20-0701E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0701A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0711	20-0711L	GCATCTCTCCACATGTGTGTA	20-0711R	TAACCTTTGCGACTTATGCGAC	20-0711E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0711A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0721	20-0721L	GATAGTGTGACAGATCTATTTGCTA	20-0721R	CAATGCGCATATGATGCTGA	20-0721E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0721A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0731	20-0731L	GCATCTCTCCACATGTGTGTA	20-0731R	TAACCTTTGCGACTTATGCGAC	20-0731E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0731A	TTCCAGAGGGGTGAAACCTTGGAGCC	
20-0741	20-0741L	GATAGTGTGACAGATCTATTTGCTA	20-0741R	CAATGCGCATATGATGCTGA	20-0741E	TTTCTAGTAAGTCTCTCTGCGACAGCA	20-0741A	TTCCAGAGGGGTGAAACCTTGGAGCC	

Table II

Table II

SNP	Name	Sequence (from 5' to 3')	Left Primer	Right Primer	Name	Sequence (from 5' to 3')	Left Primer	Right Primer
20-0751	20-0751	GAGATCAGATTAATGKATUAT			20-0751	20-0751	GTCAAAGAGCGCTCACACAT	
20-0761	20-0761	GTTCACATCCAGAGACGAATCCG			20-0761	20-0761	AGGCTCATGCTTGGACACCTAA	
20-0771	20-0771	TGGGAGGAAATGTTTATAAAGCAT			20-0771	20-0771	AGAAATTTTCCACCACTATGCTG	
20-0781	20-0781	GGACCTGGGTGCGAGATCAAAAC			20-0781	20-0781	AGCAGACTCCAGCCATGGAAGGTAG	
20-0791	20-0791	GGCCATGGCATGTGTTTCAAGAGT			20-0791	20-0791	ATGCTTATGTTTGGAGAAAGAA	
20-0801	20-0801	GGATCTAGAACAGCCCTAGT			20-0801	20-0801	TCACTCCCTCTTGGAGAAAGAA	
20-0811	20-0811	TAACCTAAACATGAATCTCTCTA			20-0811	20-0811	ATAGTGGGCGAGTCTGGGTA	
20-0821	20-0821	CATTGGTAGATGGGTCTGTGA			20-0821	20-0821	ATGCACTCTCTAGGGGACAG	
20-0831	20-0831	TCCAGGCTTGTAAATACGTG			20-0831	20-0831	CTGGAATGTTCTTCTCAAGTA	
20-0841	20-0841	CATCCTTCACTGACTGACTGATAGT			20-0841	20-0841	TTTCCAGACACATTAAGT	
20-0851	20-0851	TGCTCTCATGTCTGGGAATAGTA			20-0851	20-0851	TCCTGGCAAGGCTCTCTTTA	
20-0861	20-0861	TGCGCCCTGAGATTTGGAACCT			20-0861	20-0861	TGGGCTCAAGCTATCTTCCACC	
20-0871	20-0871	TCTTGCCCTGCGATGATCTTAA			20-0871	20-0871	AGGAGCTCCATCTCCCAAGACTAA	
20-0881	20-0881	GGTAGCCAGTGCATGTTGAGCCT			20-0881	20-0881	GTTTCTCAGCCAGTGGAACT	
20-0891	20-0891	CCACTGTGCCATATCTCTG			20-0891	20-0891	ATTATGGCACAATAATGCTGTAC	
20-0901	20-0901	GAGATCAACACTAACCACTCTA			20-0901	20-0901	TGTTTCACTCAAAACCTAACTAA	
20-0911	20-0911	GTCTGTGACATGTTTCCAGAGGTTA			20-0911	20-0911	CAACTACTTCAAGAAATTCACAT	
20-0921	20-0921	TCCACAAAATGGGAGACT			20-0921	20-0921	GGGTAGTTGGCTGAGAGTCC	
20-0931	20-0931	AGTCTGCACTGAGGAGGCTTA			20-0931	20-0931	AGGCTCTAGACTATCAAGCACT	
20-0941	20-0941	CGAACTAAACTTACATGGA			20-0941	20-0941	GGGTAGTTGGCTGAGAGTCC	
20-0951	20-0951	ATCTCCATCTGAGCATATTAATA			20-0951	20-0951	AGGCTCTAGACTATCAAGCACT	
20-0961	20-0961	TOATGAGGAATACATCATTAAC			20-0961	20-0961	GGCTCCGCTGTTTGAAGTAAT	
20-0971	20-0971	CCAGGCTTGGACCCCGTTA			20-0971	20-0971	TGAGTTTGGAGGAAACAAAC	
20-0981	20-0981	CTGATGAGATGATGATCAAC			20-0981	20-0981	GAGGCTCTGAAATGGGACCTT	
20-0991	20-0991	TCTGAGCACTGGGACTTCT			20-0991	20-0991	CTGAGAGGCCAAAGAGTAC	
20-1001	20-1001	CCGCTGTGTTATGCGCCCTCGTG			20-1001	20-1001	ATATTTGCAAAATTTGCAACCTT	
20-1011	20-1011	CACATGACACAGAGTCTTAT			20-1011	20-1011	CTGAGAGGCCAAAGAGTAC	
20-1021	20-1021	CCCTCTCAGAGGCTATGTAACA			20-1021	20-1021	GGGATGAGGCAATAAAGTGTAT	
20-1031	20-1031	AGTGCAGGATCTTATAGGGA			20-1031	20-1031	CACCTTGTGAGTATCAAACTTA	
20-1041	20-1041	AGGTGCACTGCTGCTGAT			20-1041	20-1041	AGGCTCTGAGAGGCACTTA	
20-1051	20-1051	GTGATGATCTTATGCGACCG			20-1051	20-1051	AGGCTCTGAGAGGCACTTA	
20-1061	20-1061	CCCTCTCAGAGGCTATGTAACA			20-1061	20-1061	CACTTGTGAGTATCAAACTTA	
20-1071	20-1071	AGTGCAGGATCTTATAGGGA			20-1071	20-1071	CACTTGTGAGTATCAAACTTA	
20-1081	20-1081	AGGTGCACTGCTGCTGAT			20-1081	20-1081	CACTTGTGAGTATCAAACTTA	
20-1091	20-1091	GTGATGATCTTATGCGACCG			20-1091	20-1091	CACTTGTGAGTATCAAACTTA	
20-1101	20-1101	GTGATGATCTTATGCGACCG			20-1101	20-1101	CACTTGTGAGTATCAAACTTA	
20-1111	20-1111	GTGATGATCTTATGCGACCG			20-1111	20-1111	CACTTGTGAGTATCAAACTTA	
20-1121	20-1121	GTGATGATCTTATGCGACCG			20-1121	20-1121	CACTTGTGAGTATCAAACTTA	
20-1131	20-1131	GTGATGATCTTATGCGACCG			20-1131	20-1131	CACTTGTGAGTATCAAACTTA	
20-1141	20-1141	GTGATGATCTTATGCGACCG			20-1141	20-1141	CACTTGTGAGTATCAAACTTA	
20-1151	20-1151	GTGATGATCTTATGCGACCG			20-1151	20-1151	CACTTGTGAGTATCAAACTTA	
20-1161	20-1161	GTGATGATCTTATGCGACCG			20-1161	20-1161	CACTTGTGAGTATCAAACTTA	
20-1171	20-1171	GTGATGATCTTATGCGACCG			20-1171	20-1171	CACTTGTGAGTATCAAACTTA	
20-1181	20-1181	GTGATGATCTTATGCGACCG			20-1181	20-1181	CACTTGTGAGTATCAAACTTA	
20-1191	20-1191	GTGATGATCTTATGCGACCG			20-1191	20-1191	CACTTGTGAGTATCAAACTTA	
20-1201	20-1201	GTGATGATCTTATGCGACCG			20-1201	20-1201	CACTTGTGAGTATCAAACTTA	
20-1211	20-1211	GTGATGATCTTATGCGACCG			20-1211	20-1211	CACTTGTGAGTATCAAACTTA	
20-1221	20-1221	GTGATGATCTTATGCGACCG			20-1221	20-1221	CACTTGTGAGTATCAAACTTA	
20-1231	20-1231	GTGATGATCTTATGCGACCG			20-1231	20-1231	CACTTGTGAGTATCAAACTTA	
20-1241	20-1241	GTGATGATCTTATGCGACCG			20-1241	20-1241	CACTTGTGAGTATCAAACTTA	
20-1251	20-1251	GTGATGATCTTATGCGACCG			20-1251	20-1251	CACTTGTGAGTATCAAACTTA	
20-1261	20-1261	GTGATGATCTTATGCGACCG			20-1261	20-1261	CACTTGTGAGTATCAAACTTA	
20-1271	20-1271	GTGATGATCTTATGCGACCG			20-1271	20-1271	CACTTGTGAGTATCAAACTTA	
20-1281	20-1281	GTGATGATCTTATGCGACCG			20-1281	20-1281	CACTTGTGAGTATCAAACTTA	
20-1291	20-1291	GTGATGATCTTATGCGACCG			20-1291	20-1291	CACTTGTGAGTATCAAACTTA	
20-1301	20-1301	GTGATGATCTTATGCGACCG			20-1301	20-1301	CACTTGTGAGTATCAAACTTA	
20-1311	20-1311	GTGATGATCTTATGCGACCG			20-1311	20-1311	CACTTGTGAGTATCAAACTTA	
20-1321	20-1321	GTGATGATCTTATGCGACCG			20-1321	20-1321	CACTTGTGAGTATCAAACTTA	
20-1331	20-1331	GTGATGATCTTATGCGACCG			20-1331	20-1331	CACTTGTGAGTATCAAACTTA	
20-1341	20-1341	GTGATGATCTTATGCGACCG			20-1341	20-1341	CACTTGTGAGTATCAAACTTA	
20-1351	20-1351	GTGATGATCTTATGCGACCG			20-1351	20-1351	CACTTGTGAGTATCAAACTTA	
20-1361	20-1361	GTGATGATCTTATGCGACCG			20-1361	20-1361	CACTTGTGAGTATCAAACTTA	
20-1371	20-1371	GTGATGATCTTATGCGACCG			20-1371	20-1371	CACTTGTGAGTATCAAACTTA	
20-1381	20-1381	GTGATGATCTTATGCGACCG			20-1381	20-1381	CACTTGTGAGTATCAAACTTA	
20-1391	20-1391	GTGATGATCTTATGCGACCG			20-1391	20-1391	CACTTGTGAGTATCAAACTTA	
20-1401	20-1401	GTGATGATCTTATGCGACCG			20-1401	20-1401	CACTTGTGAGTATCAAACTTA	
20-1411	20-1411	GTGATGATCTTATGCGACCG			20-1411	20-1411	CACTTGTGAGTATCAAACTTA	
20-1421	20-1421	GTGATGATCTTATGCGACCG			20-1421	20-1421	CACTTGTGAGTATCAAACTTA	
20-1431	20-1431	GTGATGATCTTATGCGACCG			20-1431	20-1431	CACTTGTGAGTATCAAACTTA	
20-1441	20-1441	GTGATGATCTTATGCGACCG			20-1441	20-1441	CACTTGTGAGTATCAAACTTA	
20-1451	20-1451	GTGATGATCTTATGCGACCG			20-1451	20-1451	CACTTGTGAGTATCAAACTTA	
20-1461	20-1461	GTGATGATCTTATGCGACCG			20-1461	20-1461	CACTTGTGAGTATCAAACTTA	
20-1471	20-1471	GTGATGATCTTATGCGACCG			20-1471	20-1471	CACTTGTGAGTATCAAACTTA	
20-1481	20-1481	GTGATGATCTTATGCGACCG			20-1481	20-1481	CACTTGTGAGTATCAAACTTA	
20-1491	20-1491	GTGATGATCTTATGCGACCG			20-1491	20-1491	CACTTGTGAGTATCAAACTTA	
20-1501	20-1501	GTGATGATCTTATGCGACCG			20-1501	20-1501	CACTTGTGAGTATCAAACTTA	
20-1511	20-1511	GTGATGATCTTATGCGACCG			20-1511	20-1511	CACTTGTGAGTATCAAACTTA	
20-1521	20-1521	GTGATGATCTTATGCGACCG			20-1521	20-1521	CACTTGTGAGTATCAAACTTA	
20-1531	20-1531	GTGATGATCTTATGCGACCG			20-1531	20-1531	CACTTGTGAGTATCAAACTTA	
20-1541	20-1541	GTGATGATCTTATGCGACCG			20-1541	20-1541	CACTTGTGAGTATCAAACTTA	
20-1551	20-1551	GTGATGATCTTATGCGACCG			20-1551	20-1551	CACTTGTGAGTATCAAACTTA	
20-1561	20-1561	GTGATGATCTTATGCGACCG			20-1561	20-1561	CACTTGTGAGTATCAAACTTA	
20-1571	20-1571	GTGATGATCTTATGCGACCG			20-1571	20-1571	CACTTGTGAGTATCAAACTTA	
20-1581	20-1581	GTGATGATCTTATGCGACCG			20-1581	20-1581	CACTTGTGAGTATCAAACTTA	
20-1591	20-1591	GTGATGATCTTATGCGACCG			20-1591	20-1591	CACTTGTGAGTATCAAACTTA	
20-1601	20-1601	GTGATGATCTTATGCGACCG			20-1601	20-1601	CACTTGTGAGTATCAAACTTA	
20-1611	20-1611	GTGATGATCTTATGCGACCG			20-1611	20-1611	CACTTGTGAGTATCAAACTTA	
20-1621	20-1621	GTGATGATCTTATGCGACCG			20-1621	20-1621	CACTTGTGAGTATCAAACTTA	
20-1631	20-1631	GTGATGATCTTATGCGACCG			20-1631	20-1631	CACTTGTGAGTATCAAACTTA	
20-1641	20-1641	GTGATGATCTTATGCGACCG			20-1641	20-1641	CACTTGTGAGTATCAAACTTA	
20-1651	20-1651	GTGATGATCTTATGCGACCG			20-1651	20-1651	CACTTGTGAGTATCAAACTTA	
20-1661	20-1661	GTGATGATCTTATGCGACCG			20-1661	20-1661	CACTTGTGAGTATCAAACTTA	
20-1671	20-1671	GTGATGATCTTATGCGACCG			20-1671	20-1671	CACTTGTGAGTATCAAACTTA	
20-1681	20-1681	GTGATGATCTTATGCGACCG			20-1681	20-1681	CACTTGTGAGTATCAAACTTA	
20-1691	20-1691	GTGATGATCTTATGCGACCG			20-1691	20-1691	CACTTGTGAGTATCAAACTTA	
20-1701	20-1701	GTGATGATCTTATGCGACCG			20-1701	20-1701	CACTTGTGAGTATCAAACTTA	
20-1711	20-1711	GTGATGATCTTATGCGACCG			20-1711	20-1711	CACTTGTGAGTATCAAACTTA	
20-1721	20-1721	GTGATGATCTTATGCGACCG			20-1721	20-1721	CACTTGTGAGTATCAAACTTA	
20-1731	20-1731	GTGATGATCTTATGCGACCG			20-1731	20-1731	CACTTGTGAGTATCAAACTTA	
20-1741	20-1741	GTGATGATCTTATGCGACCG			20-1741	20-1741	CACTTGTGAGTATCAAACTTA	
20-1751	20-1751	GTGATGATCTTATGCGACCG			20-1751	20-1751	CACTTGTGAGTATCAAACTTA	
20-1761	20-1761	GTGATGATCTTATGCGACCG			20-1761	20-1761	CACTTGTGAGTATCAAACTTA	
20-1771	20-1771	GTGATGATCTTATGCGACCG			20-1771	20-1771	CACTTGTGAGTATCAAACTTA	
20-1781	20-1781	GTGATGATCTTATGCGACCG			20-1781	20-1781	CACTTGTGAGTATCAAACTTA	
20-1791	20-1791	GTGATGATCTTATGCGACCG			20-1791	20-1791	CACTTGTGAGTATCAAACTTA	
20-1801	20-1801	GTGATGATCTTATGCGACCG			20-1801	20-1801	CACTTGTGAGTATCAAACTTA	
20-1811	20-1811	GTGATGATCTTATGCGACCG			20-1811	20-1811	CACTTGTGAGTATCAAACTTA	
20-1821	20-1821	GTGATGATCTTATGCGACCG			20-1821	20-1821	CACTTGTGAGTATCAAACTTA	
20-1831	20-1831	GTGATGATCTTATGCGACCG			20-1831	20-1831	CACTTGTGAGTATCAAACTTA	
20-1841	20-1841	GTGATGATCTTATGCGACCG			20-1841	20-1841	CACTTGTGAGTATCAAACTTA	
20-1851	20-1851	GTGATGATCTTATGCGACCG			20-1851	20-1851	CACTTGTGAGTATCAAACTTA	
20-1861	20-1861	GTGATGATCTTATGCGACCG			20-1861	20-1861	CACTTGTGAGTATCAAACTTA	
20-1871	20-1871	GTGATGATCTTATGCGACCG			20-1871	20-1871	CACTTGTGAGTATCAAACTTA	
20-1881	20-1881	GTGATGATCTTATGCGACCG			20-1881	20-1881	CACTTGTGAGTATCAAACTTA	
20-1891	20-1891	GTGATGATCTTATGCGACCG			20-1891	20-1891	CACTTGTGAGTATCAAACTTA	
20-1901	20-1901	GTGATGATCTTATGCGACCG			20-1901	20-1901	CACTTGTGAGTATCAAACTTA	
20-1911	20-1911	GTGATGATCTTATGCGACCG			20-1911	20-1911	CACTTGTGAGTATCAAACTTA	
20-1921	20-1921	GTGATGATCTTATGCGACCG			20-1921	20-1921	CACTTGTGAGTATCAAACTTA	
20-1931	20-1931	GTGATGATCTTATGCGACCG			20-1931	20-1931	CACTTGTGAGTATCAAACTTA	
20-1941	20-1941	GTGATGATCTTATGCGACCG			20-1941	20-1941	CACTTGTGAGTATCAAACTTA	
20-1951	20-1951	GTGATGATCTTATGCGACCG			20-1951	20-1951	CACTTGTGAGTATCAAACTTA	
20-1961	20-1961	GTGATGATCTTATGCGACCG			20			

Left Primer		Right Primer		Probe on Slide			
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')		
22-008L	CCCCAGGCTGACTCAGAGATGTG	22-008R	GAGGCTTCTCTAGACACTGGC	22-008E	GGCTCGGTGGGTTTGCCTAGGGGA	22-008A	TCCCTCAGTGCAGAAACCCAGCGAGCC
22-015L	TTGGAACTTATTAACACTTCG	22-015R	TGTCAATGGCCAAAACATATCTCAT	22-015E	GATTTCTGTTGGGATCTCAGGATCCAG	22-015A	CTGATCTGAGATTCCTCCCAAGCAAGAAATC
22-016L	CCCAATGTGAGGCTCTGGGCAC	22-016R	CAAGCTATGCATTAAGATTATG	22-016E	TCCAAATAGAGAGCCCAAGATGCTCATG	22-016A	CATGAGGAGCTCTGGGCTCTATCTTGGGA
22-018L	TCACTGATGGTCACTTGGTCTC	22-018R	GTTACGCTGTGTACCCGTGA	22-018E	CATAAAGAAATTTGCAGATGAAGAAACAAG	22-018A	CTGTTTCTCACTGTGACAAATTTCTTTATG
22-019L	TCAAGAGACCTCTCTCTTCACAG	22-019R	GAGGGGCTCTTCTTCTCTTGCGCA	22-019E	GTACACACTTCCAGAGTGGGGAATCTG	22-019A	CAGATTTCCCAACCTCTGGAAGATGTGAC
22-020L	TCAAGTGAATCTCTCTGCTCAAC	22-020R	GGGGCTGACATATGCAATTC	22-020E	AGAATCTTAATACAGTCAAGTGACATGG	22-020A	CCAGTGCATCTGACCTGATTAATGAGATTCT
22-021L	GAACTCCAACTCTTCTTCTATCT	22-021R	AGCAGTACAGGCAATGAGCCAGGTAT	22-021E	AGATGAGAACCAAGCTTAACAGCCCAAG	22-021A	CTTGGGCTGGTTAGCCTGGTGTCTCATCT
22-023L	GTGCAAGGCGAGATGCTCAACAC	22-023R	TGTTTCTCTTGGAAAGTGC	22-023E	CTCAACAGGAAATGGAATCAACAAATC	22-023A	GATTTTGTGCTCAATTTCTGTGTTAATGAA
22-024L	GGAGAGGATGCGGCAAGATTA	22-024R	AGGCTGCTCTCCAGTTCTTAT	22-024E	TTCATTTATCAACAAATGTGAGCCAAACCA	22-024A	TGGTTTGGCTCACAATTTGTGATTAATGAA
22-025L	CAATCTTTCTTCTTTCTTCAACAA	22-025R	GTAATCCCACTTCCAGCTCTC	22-025E	ACAATGTCTCAACCCAAACTACTGACTA	22-025A	TAGTCAGTAGTTGTGGCATGACAAATGTT
22-026L	TATGTGTAGGGTTGATGTTACGTTGTT	22-026R	GAATTGCCATATATACCTGTA	22-026E	CTCTAGTCTAGCTCTCTCTTTCCATTAGA	22-026A	TCTAATGGAAGAGAGAGCTAGACTGAGAG
Left Primer							
Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')	Name	Sequence (from 5' to 3')		
22-027L	GAGCTGTTTGTATGTTGGCAGTAG	22-027R	GATTTGAGAACCTTGAGTTTCAAG	22-027E	AGACTTCCCTGCTGATAGTACAAATTTATCAGC	22-027A	GCTGATAAATTTGATCTAGCAGGAGAGTCT
22-028L	AGTAAAGGTTAACTTGTACTCTCTT	22-028R	CAGTTTACAGTGAATTGCCAGTA	22-028E	CTTCACTACCATTAATCTCTCAATGGGCA	22-028A	TGCCCATAGGAGATTAACATGTTAGTGAAG
22-029L	CGGGGTTTCTCCATGTTGGTC	22-029R	GGGCTCACATGTTAAACCTTA	22-029E	TCCAAGCACTCGGCTGGCCAGG	22-029A	AGGCTGCACCCGGAAGTGTCTTGGGA
22-030L	TGGCTGATGTTAGATGGTGTGAGCAT	22-030R	ACCAAGCTGCTTCTGCGAGCG	22-030E	GGGAGACTGTGGGCTGTCTGTCTGCAAGCT	22-030A	CCTGTGCACAGCAACAGACTCTCC
22-031L	CTGCTCTTCTCCCAAGACTCA	22-031R	AGGAGCTGCTCCCAAGCAGGGA	22-031E	CAGCCACACAGACTACTCTTCTTCAAGGAGA	22-031A	TCTCTGAAAGGAGTACTGTCTGTGTGCTG
22-032L	CATGGCAGAAATCAAGCACTT	22-032R	CTGATGCTGAGCCGATCAG	22-032E	GTCTACTGAGCACTACAGAACCATATGGG	22-032A	CCCATATGTTCTGTAGGTGCTCAATGAC
22-033L	CTGGAGATAAAGGCTCTCAGATTTAT	22-033R	GGACAGCAAAATGCTGTGTAACA	22-033E	TATGACTTACATGATGATGAGTAATTTGCA	22-033A	TGAACAATTCAGTCAATCATGTGATGATTA
22-034L	TTAGTATGTCTCTTCTCACTCAG	22-034R	CTCAAGGCGCTTACATCTTAA	22-034E	TCTCAACTAGTATTTCTCAGCTAGGACAT	22-034A	ATGCTCTAGCTGAGAACTACTAGTTGAGA
22-036L	TGATGGGTTGTTGGAGTTGACAA	22-036R	TGCTCTGTTTGGTCACTT	22-036E	AACACTGATTTAGGCGCTTTGATCTCA	22-036A	TGGAGATCAAAAGCGCTCAATGATGTT
22-037L	CAAGATGTAGAGGCACTGCTGTA	22-037R	TTGAGGCTTGAATTTCAATTGA	22-037E	TGAATAAACAAAGAGCAAGCGCTGGGCT	22-037A	GAACCCAGCGCTCTCTTGTTTTATTTCA
22-038L	AGACCCCAATACTGACAGTCAATC	22-038R	ACTGTCTCAACCTGGAATGTGAT	22-038E	CAAGTGAATCACTAGTGAAGTATGAC	22-038A	CTGTACATGCTACTGATGATGACTCTTGT
22-039L	TGAGAGATTTGGGACCTTTTAAACA	22-039R	CTGTCCGACAAAAATCCATCTCT	22-039E	TTTAAACATTTTCTACAGAACATGTCGCG	22-039A	GGGCACTGTTTCTGTGTAAGAAATTTTAAA
22-040L	TTGGGAACTGTCCCAAGCTCTC	22-040R	GGTCCCAATATATTTTCCATGAAT	22-040E	CACATAGCTCCAAATGTTGTTTCTCTCTCT	22-040A	GAGAGAGAAACCAATTTTGAAGCTATGTT
22-041L	CAGCCCTGACTGCAACTCTC	22-041R	CCCAAGGCAACCTGGGTGA	22-041E	ATGCTCAACAGCTCTGTAGGGGCTTCC	22-041A	GGAGGCCCTTAACAGACTGTTGTGAGCAT
22-042L	CCCAATTAACCTATGAATAG	22-042R	CCCTCCCACTGGCTTGGCGAAT	22-042E	GAAAACTGAAGGCTACAGAAATTAAGACA	22-042A	TGTTCTTTTAAATCTGTAGCTTCAATTTT
22-043L	AGGGCTTTGGCACTGTTGATGAGG	22-043R	GGCTTACAGATTTTGGAGCTCT	22-043E	GTTTCAATGTCGGAAGATGCAAGACACTT	22-043A	AAATGCTGTGATCTTTTGGCACTCTGAA
22-044L	GGGGGAGGAGGCCATGCTC	22-044R	ACTGAGCTCTGTAGCGCTCAATG	22-044E	TCTGAGCACTGCTCTCTCAGAGCAT	22-044A	AAATGCTGTGATGGAAGAGTGTCTCAGA
22-045L	TCTGAGCCAACTTTAAACATCTT	22-045R	GAAACAGATCCCAAGCAGCTCTT	22-045E	GGCCTTGGAGCTGTGGAAGCCACTG	22-045A	CATGGCTTCCAGCTCTCCAGCGCC
22-046L	TTTAAATGCTCAATTTTGGTTA	22-046R	CTTCAAGAAATATTTCCGCTGA	22-046E	TTCCTTACCAAGCTTTCCAATTAACATTTG	22-046A	CAATGTTTATTTGAAGGCTGTTGATAGCGAA
22-047L	AGGTGTGCACTGTCCCTCAAGCG	22-047R	AGAGACTGTTTACCAAGCAAGCG	22-047E	TGCAGCAGCAGGGCCAGTCTCTG	22-047A	CAGGACTGCCCTCTCTGGCTGCA
22-048L	TGGAAGCACAGTCCATGA	22-048R	AGAGCCAGAACTTGGCCACAC	22-048E	GTCCAGTGAACAGCAGCACTGTGAACAAA	22-048A	TTTGTTCACATGGCTCTGTCTTCACTGGAC
22-049L	CCCTGCACTTACTTGCCATGAC	22-049R	AGTTCTCAAAATATCTATGTGTT	22-049E	ATATGATTTTGGGAAAGGATGACACCC	22-049A	GGGTTTCACTGCTTGGCCAAAGTATAT
22-051L	TTCCATTTCAATATCCCTTTCTA	22-051R	TCAAGTTACAGTCCCTGGAACC	22-051E	TTAAAGTGTTTGAAGACAGCTGGGAACAC	22-051A	GTGTTTCCCAAGCTCTCTTCAACACTTTAA
22-052L	TOAATTAAGACTAGCACTCTTGGGA	22-052R	ACAGAAATTACTCATGGGATG	22-052E	CTTGGACTCTCACAATAAAATCTGATCT	22-052A	AGCATAGAAATTTTAAATGTGAGAGTCAAG
22-057L	CATGACAGAGCAACACTCTT	22-057R	TCCTTTCTGTCTCTCTATGT	22-057E	GGAGGCGGAGCCAGGCGCTCTGTCT	22-057A	GCAATGTCTCTTAATGTGAGCTGGCTGATCT
22-059L	GGTGGCCAGGGGCAAGAGATA	22-059R	CTGTTCTGGCTTCCATTC	22-059E	CATGGAAGCTGGTCAAGTCTGGAGCC	22-059A	AGACAAGAGCCCTGGTCCCGCTTCC
22-060L	GAAAGGAGCCCACTACAGGGACAG	22-060R	CAGTATGGGAAGCAAGGAAGAAA	22-060E	CATGGAAGCTGGTCAAGTCTGGAGCC	22-060A	GGCTCTGCACTTGACAGCACTCTTCC
22-062L	CTTCCACATTCCTTGGATG	22-062R	CAGTATGGGAAGCAAGGAAGAAA	22-062E	CATGGAAGCTGGTCAAGTCTGGAGCC	22-062A	CTTCTGTTCAGGAGCGAGGTCTGTGACC
22-064L	AGTGTGTGATCATAGCTCA	22-064R	TTAGCCAGGCATCTGTTGTA	22-064E	GTACACATATAGTCTCAGCCACTCAGGAG	22-064A	CTTCTGATGTGGCTGACACTATATGTGAC
22-065L	TACTGGGATGGGCAAGGATGACGG	22-065R	CTTGGGCTCTTCCAGGGCAACT	22-065E	GGAGGCTCTCGGCTCTCACTCTCTCT	22-065A	AGGAGGTGAGCCGACAGGTGCTCCG
22-066L	GAAAGGACACAAATAGCTACGTAT	22-066R	GACAAATATTCAGCGGAATA	22-066E	CAAGGCTCTTCAAGCACTCTCAGGAG	22-066A	TCCACATTCATGTCTTATGCACTGTTC
22-067L	GTAAATGAGATGGACACATAG	22-067R	AGAGCACTCTGAAAGATTAATG	22-067E	TCTGTTGTGCTTCTGTTGGCATGGATAC	22-067A	GTATCCATGGCAACAGGAGGACAAACAGA
22-068L	AAGGGCTGAGGAAGAACTAAGAGACC	22-068R	AAATATCCCACTCTGTGAAATCTG	22-068E	TTCCGAGCTTGAATGGCACAGTACTCTG	22-068A	CAGATGTACTGGCACTCAAGAGTGGGA
22-069L	TGGCTAGTTGCTGCTGTTA	22-069R	ATGCTGAGGAATGCGAGTGTGTCG	22-069E	TTCGAGGCTGAGTGTGTTGTGTCG	22-069A	GCCCAACAAACTCTCAGCACTGGAGCC

Table III 627 single nucleotide polymorphism (SNP) markers

Note: In each block: First part of the first line, Name of the SNP; Second part of first line sequences length shown; G/A or alike, polymorphic site showing nucleotide sequences variation; Other parts, nucleotide sequences flanking the polymorphic site.

01T002 132bp
CACGTGTGAG GCCTTGGTCC CCACCTGTGG ACTCAGGGTC TCTTTCAC
G/A
GACTGCGGGG AAGGCAGTGG GAGCAGCAGG AATGGATGGT GAAAGGACAC AGTGCCCGCC
CCCCGAGTGT CCGAGGGTAG AGC

01T003 145bp
CTATAGCCCC TCTGAATGGT CTGTGACACA TGCATGCTTT CAGCTATTCT CTCTATAGCC
CTTCTGAAC
A/G
GTCTGTGACA CCATTATGCT TTCAGCTACA GTTTGCTTTC TCTGGTTTTT CAGTGGTGCT
CTGGGGAAGG CAGAA

01T006 141bp
AAAGAAGAGA GGTTTTTGGG GATATTTTTA ACACATCTAT AATCTTTCAT TAACAGCTAG
AAATTTAGAT TGC
C/T
GTACATAAGT GATAGACAAT GAAACAGAGA AGGCATTTCT GAGAGTCTCT CGGCTGTCAG
CATTGTG

01T008 147bp
ACTAAGGAGG CATCAACAAC TCTCCCAGCA GCTGATGGAG GATGGAACC ACACAAGTGC
GGAGATTTC A GGTGGGGACT TGGTGGGGGT CGTGTGAGCC
C/T
AGGGAGAGAG GACGGAAATT CAGCAAGGAC GTAGAAGAGA GTGCTT

01T009 130
GTACGGTGCT ACAGGACCCA ACAGAGCCAG AGACTTGACC CAGGTC
A/G
TTTAGCCACC CAGCCCCAAG CCAGCAGGGC CAGCCAATGG GAGCCTGTGT CCCACCTCTC
GCCCCACTC AGACTGTGCT CCC

01T012 138bp
CAACTTGAAG TAGTAGGTAT TGGAAC TAAG AATGATATAA ATAGAAATTA ACAATTC
G/A
GAGATTAGAA TAAGGTGCAG GAAATTACTC TGCAGTGTA TTTTGT TTTT CTCTTAATTC
AAGAGAGCTT GGAATGCTA

01T013 131bp
GAAATTCTAT CTCACCACCG TGAAACTCTT CAGTTTTCTA ATTGCTTTAT CAGCAGGGGG
TATAAAAGGT
C/T
ATGAAAGCAA TTTCCACATG CTGTGGCTCC AGGTCTCTGG GTGTGAAGCA GAGCAAGCCT

01T014 140bp
ACAGCCTGTC ACAGAAGTCC TCTTTGGACC AGATAGGGCT GCCTCACAGG GGTTCAGTT
TGTCAATTTCA
A/G

TTCAACAAGT CCTGAACACT TACTCTGTGC CAGGAATTTT GCTGGGCATT AGGGATCCAG
AGAAGAAGA

01T019 139bp
ACTGGCCACC TCTGCAGAAG CTAATTGTCC AGAGGAGGGA AAATACAAGT TTATAAATAA
CTAAAATATC AGGTCAAGCA CATTGCAGG
A/G
AGCAAAAGTG GAATAGAATA ATGGGGCTGG GAGCTCCAGG AGGAAGAAC

01T020 147bp
AACACCTTGC CTGGCATATA GTAGATACTC AATAAAATCT CTGTTGGATG ACTGAGTTTA
GGCTGAGGGA GAGGGAGAAG AGGGAGGCAG GGAA
G/A
CAGGAATGTC TGGGTCCTTC TTAGGCTCTC ATTTGAGTGT CCTCATCCAT TC

01T023 131bp
AGATTTTCTT GACCGTCTTC TTATTCAGAA TTCATCTTAA ATAAATGTCA CCTCCTCAGA AT
A/G
GTCCTCCTTG ATTGCACTGG CCAAAGCGGC CACTCTGCTC CCCAAGTCAC CGTTGAATCT
ATCCTTTT

01T025 138bp
AAGGGATAAA CCTCACTGAC TTGGAGGAAA TCAAGAGGAG TGAGCACAGC ATCAGAAAGC
CCCTGGCCC CAGACTGCAC CC
G/A
CTTTCCTGGC CCTACCTTGA AATCCATCAG GTCTGCGTTG GACACGGCAT TGTAC

01T028 146bp
CCCAGCGGGA AGCTGTTGAA ATAGTTCAGG GGAGACGGGA GAGGTTCTGG ACCAGGGCAG
GGCAAGGGCA GAGGGGAGGG TT
C/T
AGGACCTGGA GCTCAGGTGG TGCTGATGGA GCAGAGAAGG GAGACAGACC CGCATGTGCT
TTC

01T029 108bp
AATTTAGGCC TTTATGTAAA TTCAGAATGA TACAGATTTA GACTTTATAT AAATTGCCA
A/G
TAAGTGGCAG AGTCAGGTCT TGAACCCAGC TGCTCTGAAT TTAAAAGCCT TTGCCCTC

01T032 101bp
CAAAAGACCT CCAAGTCTTA AAAAAAAGA CCTCAAAGGC CTAAATCTGT TCAAAGCTTC
A/G
AGGTATTCGG CAAGGATCTC CTAAACTCTT TTTTGTCTT GGTGGTATGA

01T035 Rsa1
GTGCTCATGA GCCGCACGGG-GCCAGCGCTG GTCCTGGGAC GGGT
A/G
CGGCCACCGG GGGCGCTGCT CAGCGTGCCC GTGCTCAGCA GCCT

01T037 122bp
CCATCAGGTA ACTGACAAAC TCTAAGGAAG CATCTCTGTT TTTCTGGCCC TGTACTAGGT
TCTGGAAGG
C/T
GGTGAGCCAG CAGGCAGGCC TGGGACTGGG AAGCCAGCAC TAGGGCTCAG GG

01T038 130bp
TCTTAGCAGG GGGAACAGCC TAGGCAAAGG CCTAGAGGCT GGAA

Table III

A/G

GGGGTAGGTT TGTATGAGCC ATGGTGAACC AAAGTGTGAG AAAGAAATGG CAGGAGAGGT
 TTGAGTCCGT TAAGAGAAGC CTTGA

01T039 130bp

CTCTCTAGTA AACCCGATCA CCTCCCACTG GCATGTGCCT AACACGTAGG AAGTTCTCAC
 A/G

ATGCCCTATT GTTAATGATG GATGACTCTA ACTATGATAG CTAATATTTA TTGAAGGCTC
 TGAGAAGCC

01T041 149bp

TCTCCAGTGA GTCTGGGGGC TGGCAGGGTG ATAACACGAG GCCAAGGCTC AGAGAACTGG
 GCCCTGGTTC CTAGGCCTGG CT

C/T

TGACATTAAA AGCAGTATGA TCTTTGTTTG ACAAGTTATT TCACTTCTCC AGTCTTCAGT
 TTCCAC

01T042 127bp

CTCACTCCCT CAGGCCTCCG CCCAGTGCTC TTTCCACAG AGGC

C/T

TACCCTGACC ACTTGATCCC AAACAGCCCC TGCCTGTCCT CCCTTCTCCC TCCCATCCAT
 CTGTTCTGCT ATCATCTTCC TT

01T043 113bp

ATTCTCGAAC TTTCACGCAC AGAAGAATCA CCCAGAGGGC TTGTGAAAAC ACAGA

T/C

TGCTGGGCCC CAGGCCCAGA GCTTCTGATC AGTAGGTCTG GCCTAGGGCC TGAGAAT

01T046

TCTGAACACC CGGTTTATAG TCCCAGTCCT GCCACTGTAG GACATTGAAT AGGTGATGTT
 ACTCATCTGA AATTGTATCT

A/G

TTTTGATAAC ATGGGGATAA TATCTCTTCT CTCTACTTGA ACAATGAGGT AACACTGATG
 ACC

01T047 147bp

CAGAGGGGTT GCCGTTGCTC CTTATCCTCC CATCATTTGA TAATGTCAGT TTTTTTTTAA
 ATTTTAAACCA TTCTAATAGG CATGTGGTAG TATCTCACTG

C/T

GGTTTTTCATT CATGTTTTTC TAATAACTAA AGATGTCGAG TGCCTT

01T048 140bp

CCACACCCTA GAAGGCTGTA GAACATGAGG ACATGAGCCA TGTAGGACGT GAGGATGA

T/C

GCCAGGGTTC CAGTGCAAGC TGAGACTTAA GGGTACCTTC CAAGAAACCA GGAGGAAAGA
 GCGCAAGGAA CTGGAGTTTT T

01T051 130bp

CTACCCTGCC TCTGGGCCTT GACCTGTGCC CTCTTCTTCC ACAGCTGTGA TTGTGGGCGG
 GGTGGTGGG

C/T

GCCCTCTTTG CTGCCTTCTT GGTCACACTG CTCATCTATC GTATGAAGAA AAAGGATGAG

01T054 133bp

TGAGATGGCC CAGACTCCGT GCAAAGGAAG GCAGGATGAG GAGGAAGTGA CC

A/G

TCTTCGTCAA GGTGCACAGA GCTGCACAGC AGCCCAGATG GCTCTGCTGA GAAGACACCT

Table III

CATTTGGAAG TAAACACAGGC

01T055 118bp
CCTGGGGCCG GTGACAGGAA AACTAGACCT GAAAGTGTGA GAGGAAAGAG AAGTTGCTTG
AACTCAGAGA G
A/G
CCTCTGTGGA GAGGGCCATC CTGCAGGAGC TGAGATCTTC CACTAA

01T056 122bp
CACAAATGGGA ACAATAAATC CAACCAGAAG GAGGGCCATG TGTGTGAGCT TGACAGTGCA
A
T/C
GCATGGGAAA AGGAAGAGGG CGGGTCTTCC TGGGTTACCA ATTCACATCC ACCACCATTC

01T057 137bp
CCCATTAGCC AATGAACAGC TTGTTTCTCT TCCTGAAAAA AGGATAGATC TTACA
C/T
TCCCAAAGAA TCAGAGCCAG ATAACAGCAA CAACTTATT GATCAGTTAC TATATGGTAG
CCATAGTTTT GTGGGTTTTT T

01T058 142bp
GTGTTCCCGG TCGGCATATG ATGAAAAACA TGGGTTTGTT CCTGGGCTAG GTCTCGGTCC
GAAGCATGAA GGGATTA
C/T
TAAACCCCTC CCAATTACTA TAAAATAAGA CAGTAATGGT TTAGATTATC CTTTTTAGTG
GTGG

01T060 130bp
GGACTGCTAC TACACAATGG AGGTAAGGAA GATTATGTCT GGAATAAAGA AGATCC
C/T
TTAGGTTATC TCTTAGTATT ATCATGGCCT ATGATTAAGA TCAATGAAAA ACCAGAACAA
CTCAATCCAG GCA

01T061 125bp
CCAGCGTTCT GCAAGGGGCT GGGTAGAAGG GGCTGGCATG GGCATCTGGA ATCCTTCAGC
CTAGTCCTCT GGC
T/C
CGGTGATGAA AGCCCAACCA CTGTTCTCAG ACCAGCAGGG ATAGTCTATC C

01T062 142bp
AAATGTGGTA CATGGTCTTT GTAGTGATGC CTGTTTTTCA AAATTTCACT CTACAAACAA
CCTCACCA
T/C
GAACTGTTGT GAGAACTGTG GGAGCTATTG CTATAGTAGC TCTGGTCCTT GCCAATCCCA
GAAGGTTTTT AGT

01T063 95bp
ATTCATCACA TAAAATGCAA CTACCCTGTA ACTCACATAT GTAAAT
C/T
CAATAGCAAG AAACATTCTG AGATTCAGCA GTGGGATTTC AGAAAGCT

01T064 146bp
GTGGTCCTAC ACAAAGAAAC GAATATTGGA AATGGCATTG AGAAAGCATG TACTACACGT
TTTCTTATAA TTAAATCTT TCAAAAAATA TTTGACGTAA
T/C
AAATAAAAGT AATAATAATG AATCACAAAG GTTATAGTGC ATAAA

Table III

01T065 141bp
GCCACTCCTG ATGGATGATC TTACTTGCTT TGCCAATGAC AGGAGTGAGA TGACCCATTT
CTAGCAAAGC CATGAGGCCG TATCTG
T/C
TGGAGCTTCC AGGGGAAGAC TTCCTTGCTT TAGAAGGACA CAGAAAAATC TGTC

01T066 148bp
TTGAAAGTTC TGGTGTATAG CCCAAAGGGG ACAGACAAGA AACTTAAGAG TCTG
A/G
AAGGGGTAAC AGGGGCTTAC GTACTTCTGT TTCTTTGATC CTTTATGAGT TTTCTCTGTT
TTTTCAAGCTG ACCTTTCCCT TGAGTGACTG GAG

01T067 143bp
AGAGGGATAC TTGTAAACTG AAAAGGCTGA GCCCAGAAGA TAATACACCA ACCAACCTCT
TTCTTA
C/T
CATTCTAGG CCCAGTGTT ATCTGACTAT TCACCTAAAA TTGTAGAGAC TCGAAGGGTT
GTGGCAAGAA CACTGG

01T068 125bp
TACAATGCTT TTCTTCAACA ATAAACAGCA AGATCAACAC ATGTACT
A/G
GTATAGCTGC TTAGCATTTT TAAGGGAAGA ATAAATTATA TGGCCAGCCA GCTAGCAAAA
TAGAGTGAGC TACCACA

01T069 131bp
TATCCCTCCT GCCATCCGTG GAAAAATTGT CTTCCACGAA ACTGATCCCT GGTGCCA
G/A
AAAGGTTGGG GACCACTGTC TTAAAGCATG CCCATAAGGG TGGGTAGCTC ACTGGACATC
TACTGAACAA TTT

01T070 131bp
TTGTCTCCTC AGGTAGTGAT GAATTAGTTG CTGTCACAAA AGGAGGGAAG TAGCACCCAA ATTAA
A/G
TTGCTTAAGA GAGGAAATGT ACATCTTGTA TAACTTAGGG AGCGAAGAAA ATGTAGGCGC
GAAAG

01T071 141bp
GGCCCCTATT CCAAGAACCA CGCTGGGCCA GGGTACATGG CTCCCTTGGA GCTTTGATGG
CACTTC
T/C
TTGGGAAACA GAAGCTGAAT GTTTAAGAAG CATCTGTCAT TATGGAAACG AAGTTGCCAG
GCCATTTTTT CTTT

01T072 146bp
TTGTTTCGTTA TGTATCACTT CTTTAAACC TCAAAGGCAG GTTGATCAGT AACCAGGAAG
AATGGATCTT TGAATTTCTG AATTCTCG
T/C
AGTAAACTT TCCGATGTCA TCCAAATCCC ACCCGAATTT CTTTTTAATT GAAAGA

01T074 102bp
ATTAGCACGT CAGCTTCTC TTGTGGTATT TATGTGTTTA TATAACA
T/C
AGTTCATTGT TCCCAAATGT TAGTCAACTC CAACTATAAA TCAAGCCCCA AATC

01T077 124bp

Table III

CAAGAGAGGT CCCACCAGGA AATATTATAG TCAAAGTGTG AAAGGCCAAA GGCAAAGAGA
AAATCTTG
A/G
AAACAGCAAG GAAGAAGCAA CTGTTTACAT ACAAGAGATT CTGAATAAGA TTGTC

01T079 127bp
GATGGGAGCC AAACATCATC CTTTTATCAG GAACCCACTC CTGTGATAAC TAACCTACTC
TCATGATAAT GACGGCAGG
A/G
CCCTCATGAC CTAATCACCT CTTAAAGGTC CTGACTGTCA ATGCTGT

01T083 129bp
CCTCTTATCT GAGAATGACC CTTCTCCCCC AAGGAGTCCC AAAAGGTGGG CTTCTTTGTT
GATTTAGAGA
A/G
TCGATAATTC AGTAAAGTCC CAAGTAAATG GCACAACACA AGCTCAGA

01T084 142bp
CAAAGGGACA AATACTGTAT GATTCTACTT ATATGAGGTA CTAGAGTAGT CAAATTCA
C/T
AGAGACAGAA AGTAGAATGG TGGCTGCCAG AGCTGGGGAA TGGGGAAATG AGGAATTAAA
GTTTAATTGG CAAGGAGTTT CAG

01T087 137bp
GCTTCAGAGC TCTGCCAGCT GCCATTCTAC AGAGGCAAGC CCCTCCGGCC CCATCTGGCC
TCCCTGACCC AGGG
C/T
GCTGGCCTCT GATTGCATTC CCCTAGTGAC AGGGAGCTCA TTAGGGCCTG GGGCTTTGGG
GA

01T088 145bp
CAACCCCAAG ACTCCCAGGC ACATGGGATG GATGTCCAGT GCTACCACCC AAGCCCCCTC CTT
C/T
TTTGTGTGGA ATCTGCAATA GTGGGCTGAC TCCCTCCAGC CCCATGCCGG CCCTACCCGC
CCTTGAAGTA TAGCCAGCCA A

01T089 146bp
ATTTACATGC ATTTAATCCA CGCAGCAAAA TCCTAGGAAG ACAGTATTAT AGACCCTATT
TTGCAGTGAG TAGACTGAGA CCTAGAGAGG C
C/T
GAGCCACTTG TTCAAGGGCA TACAACCTACC TGGTGGGGGA ACAGGACTGG AAAC

01T090 147bp
CAGCATGTTA TAAATGCTAT ATGGAGTAAT AAGTATGGTA AGAGAATAAT GATTGAGGGT TGGG
A/G
TTACAAATTTT AAATTGTGTG GTCAGGAAAAG GTGACATTTG AGCAGAGACT TCAGTGAAGT
GGGTAAGTGA ACCATGTGGA TC

01T091 147bp
ATTTGGAGCC ATAAAACATA TCTAAACTAA TTTAAAAGAA TGGAATTCAT ATAATGTTTA
CTCTCTGGCC ACAA
C/T
GGAATGAAAC TAAAAATAAG TAACAAAAAG TTACCCAGAA AATCCCCAAA TACTTGCAGA
TTAAACAACA CA

01T094 112bp
TCGAATCTCG CCCAAAGTGA CGAATAAATC CGGACTCTCA GCAACATGGG CTATAGGGAG GATCC

Table III

C/T

TAAGAATTCC TCAGTGACCA GATAACTCTG TGCATAGACC AAGGTA

01T096 116bp

TCAGTGCCAG AAAGATGTGG CTTAAGTTCC TGCGACTCCC TTAATGTGGA GCTCAGACAC T

T/C

GCCATGGGGA GAGCCAAACT GCCTTCACAG CACTAGATGC TCCATAAGGG ACCA

01T097 148bp

CAGGGTCCCT TTCCGTAGAG CCGCCAAGTT CTGGTTCCTT GTGGGTCCCG C

C/T

ATGCACCTTC CATCCATATG TGCACATACC AATGTGCAGC TCTTTTATT CATGTAGTGG

ATTCGGATCA CACATATAAT ATGCCTGTGA CGACTT

01T098 134bp

GGCCAAGGTA TAATCACACT GGTAGCTGGA AAGCCTTCTG GGCTGGGGTG CCATAGGCTG

T

A/G

TTTGGGTTCC AGTTCAGCG CTGACTTTGC TCTATGATTC TGGACAAGTC ATCGCCCTCT

CTGGGCCTCA GT

01T099 145bp

CCATTGCTGT GTCCAGGGC ATTTGGCAGC ACGGCTGGGT GGTGAC

A/G

AGGCCAGGAG TAGTATGTGC AGGCACAGGG TGGGCGTGGC AGCTGTCACA TGGCAGAGGA

CCCGCAGAAG CTGCTGATGG CTGGAAGGTA ATTAACA

01T102 130bp

AAGAAGCCAG GTACCAAAGA GTACATACTA TGTGAATCCT CTTAACATGG AATTCTAGAG

CAGGCATAAT GGTCATAGTG AC

A/G

TAAAGCAGAC CAGCGGTTGC CTAGGGTGAG GAGTAGGTGA TGGGAGG

01T103 148bp

GACAGGGTGA TCAGGACAGC TTCTATAAGA AGGTGAGGTA TGAATTAATG C

C/T

TAAAGGAGGG GTGAACATGA GCTAGGCCAA TTGCAGGAAG AAAGGGTCAC CAATGAAAAA

GCACAAGCTA GGATACATCC CAGGAAAGAG CCAGAT

01T104 109bp

CTGGGAAGAC GTCTCTTCAA AGCTATTTGA AAGAACTGTG CTTTA

A/G

GAGATAAAAT ACCTAAACAA GCAAATCCTC AATTTCTTTA CACAGACTTT CTGTCATTAG

TGT

01T105 140bp

AAATGTCTGC AGTCTGGCCT CTGTCCCCTT GATGCCAAAC AAAAC

C/T

GCCCTGCCCCA AGGTCACCTG TGTAATCTA AATGACACCC CTCAGCAGCA GTGGGAGCAT

TCTGTCCTGG TGTGTTCTCT GACTCTGTGG CCTC

01T108 134bp

GGATGAGAAG GAAACAAGCC TGGTGAAATG GAATGGTCAG AAAAGCCTCT

C/T

TAGCATAGTA CTAATTACGG GGTAAATTC ATGAGGAGCC TGATTTGGAA GTTCAAAAGA

GGCGAGAAAC TAGACAGAAT GAA

Table III

01T109 107bp
 CATTGTGTG CTTGTCTCCC TCAAGAATAG GGACTTCTCA AAAATCAAGC TACATGCTGC
 AAGTGCTTGT ACC
 C/T
 AGAGCTCTGA ATCTGACACA AAGTAAGGTT CATACGCATT CAA

01T111 122bp
 GGCTTATTTG ATGGAAATGG TAATAATGAT AATAATAACC ATGAACCTAC TGAATATGAA
 ATATATTAAT AA
 A/G
 CCATCTTAAA ATGTTATTTA CTCTTCACAA CAATGAGAAA AATGTGTAT

01T117 144bp
 GTCTCCATCT CTCTTAAAGG AAAAAAGAC GACATTACAC AGCAACATGA TTATTTAATT
 AATAGCTTTT CC
 C/T
 TTTGATGCCA GTCTTGTTTT AGTTATAATA AACTAATAG GTATATCTGT CAAAGGACTT
 ACAAATAAAA G

01T118 126bp
 TGCCAATCTT TCTGGCAAAA TCAAAAATGC TTCCAAACCC AGGGAAGCAG
 T/C
 ACTACTCTGT GTGAGAAGTT CTGTATAAGC ATAGCTATCC CTAAATGCAG GCTAGCAACC
 ATCTCCCATC ATAAA

01T119 143bp
 GCCAGAGGCT GATGGCAGTG AACAAAACAG ATGAGTTATA GCTTTAC
 C/T
 AGTTGGTGAA AAAGAGAGTT TTTAAATAAA AAGTTATACA ACTAGATATA ATTATAAATC
 ATGTTTACAG AGTTATGTGT GAGAATTAAA AGGGA

01T120 142bp
 CCTATAATCC CAATGCTTTG GGAGGCAGAG GTGGGAGGAT TGCTTGAGGG CAGGATTTC
 AGACCAGCCT GGGCAATATA GCAAGACCCC ATTTC
 C/T
 ATAAAAAATT TAAAAATTA GCCAAGAGTG GTGGCAGGCT CCTGTA

01T121 120bp
 GAGGCAGGGT AAGCAGGATT CAGATTGGCG AGTTGGAATA CTTTCAGCAG GCTCAGGGCT
 GGCTGTCTTT AGTTGTC
 C/T
 GGTACCTGGG CCTGGGGTGA TTAGAGGCGG GGAATACTGG CC

01T127 140bp
 GGAGCTGCCC AGAAACAGCC TTGTGGGGTG GGGTTGGTGT CTGACCT
 T/C
 CCTCCCCGGG GGCCTTCGCA GGCTTCTCTG CTGGTGCTTC TGTGCCTGTG GGTCTGGATT
 CCTCCAGGGC CTGATCCTGG GTGCAGATGC AG

01T128 142bp
 TCCCAGGGGC TTCTGTGGCC TGCTGAGGCG CAGTGGGGGA GGCTGGCAGA GGCAAGAGGG
 CAGGGCCTGA GGGATGG
 A/G
 GATGGGAGGC TCTGCCTCTC ACATGTCCTG TCCTCTCCAG ACCCCAGGGC TCCGTCCTCT
 GGAC

01T129 141bp

Table III

ACCCAATATG CCAGTTAATA CTGACATTTT CAGTGGGAAG GGAAGAGGTG AGAAGATAAC
ACCTGAGTGG GCTGATGAGC C

A/G

GAACAGTTTA AGTGGGGGAA AGGTCTGGCA TTGCCTTAGA GCTGGTGACC AGACTCCCC

01T131 133bp

CCTGTTATTT TCCAGAATAA TCAGTGATAC TCTGTGATAT TGATAATCTA CTTGTTGGC
CCTTACCAA

A/G

TTACTGGGTG TGAGTAACAG CTGACTGTAG CTCCCTTTCT CTACCCTAGT GCTCTGGAAG
GAG

01T133 126bp

AATCTACCAA TCTGACAAAG GGCTAACATC CAGAATCTAC AAAGAACTTA AACAAATTTA
CAAGAAAAAA ACAACAA

T/C

CCCATCAAAA AGTGGGCAAA CAATATGAAC AGACACTTCT CAAAAGA

01T135 129bp

TTAAAGTCTT TTATGCCTTC CCACCCATCA TTAAAAATTA ATAAATTTTG TCACTCAGCC
ATTTACAAAA TAATCTGATA

C/T

TACAGATTAT TTTATTTTCT TCTACAAGAA AACCATATCC TATTTCT

01T137 148bp

AAAAAGGAAA CCACCTTCT ACCAGGGACC CTTAGATCGA CCCCAGGAGG AGCCCTAGAT
GCTGTTCCC

A/G

TACCAGCCCC TCTCCAGCGG GAAGTAGCCA GAAGAAGTTG TTGCCCAATT CCCCCTAACA
GCAGTTAGGG ATTCCATT

01T138 105bp

GAAATGATTC ACACCAATTC ATGATAGAAG GTTGCACTTG C

A/G

GAGGGTTGGT GTATTAGTCC ATTCTCACAC TGCTACAAAG ATACTACCTG AGACTGGGTA ATT

01T145 149bp

GGCAGCTGGA GGTTAAGCAT CTAAGATTAA TTCCTGAACA CCAACATAGA AAGGCCAC

C/T

AAGGGAGTTG CTGCCTGTCT GATCAGGAAG CTTCTGGAGT CAGGAGCTGC TTCTTTAGTT
CCTGGTTCCA GGATCATCCC AGCTCTGCTG

01T146 127bp

ATGTGTTAGC TCCCACTTGT AAGTGAGAAC ATGTGGTATT TGATTTTCTG CTCCTACATT
AATTTGCTTA GGATTATG

A/G

TCTCCAGCTA CGTCCATGTT GCTGCGAAGG ACATGATTCA TTCTTTCT

01T147 140bp

AATATGATGA AGCGTAGTGA AACACATAT GTAAAATGTT ATTTACA

A/G

TGGCAAGTAC TTGAGATACA TTCAGTAATG AAGGCTATCA TCATTGTTAA TGGCAGGAAT
TTTCAAGTGA GTCATTATGT TTACATGCCA CA

01T148 102bp

AGGAAGGAAT AATAGAGAAA CTTACCCAC TTCTTTGATA AGTAGGACC

G/A

Table III

GACTCCATGA GCCATTGATT ACTTCTTGTG TCAGACTGGC ACATATCAAG GA

01T150 100bp
TCAGAAGAAT CGTTTGAACC CTGGAGGCAG AGGTTGCAGT GAGCCGAGAC AGC
A/G
CCATTACACT CTGGCCTGGG CAACAGAGAG AGACTGACTC AATAAA

01T151 126bp
GTACATTGGC CCCTTTTATC CATAGCTGGA GTGGCTGGGA CACAGGACAC CAA
G/A
TCCCTAGGCT GCACACAACA CAGGGACTGT GGGCCCAGCT GATGAAATCA GTTTCCTCCT
GGGCCTCTGG GC

01T152 134bp
TTCTTCTAAC TTCATACTGG CTTGTTTGTG AAAGAAAAGT CTTTGAAAAG GCTACCTG
C/T
AGGTGATAAA GATTTTTTAAA GTATTCTTTT CTTCTTTTTT ATTAGAGAAA ATCCAAAGGG
AGTTTTAAAA TTTGT

01T153 141bp
ACTGGATTAT GCTCCAGGTA TCTGACAGGT TTTCAATACT ACTA
A/G
TATGTTTATT ATAGCATAAA AGGGCAATAT AAAAATAATT AAGAACATCA ACTTTATAAT
AAACAAGACT AGATATTGAA TCCTTGCTCTG CACTTC

01T154 117bp
CCATTCTTCC CGTTAAATA GCAAAATCAA GGATACTAGA ATAATGTATA ATGTGTTCAA
CACTAAATCG
C/T
ACCTTCGAAT TTATATACAG TTTTAAAGAC ACTGACCCTA AGGAGA

01T155 149bp
GGATAACCTG ATGAAATTCA AACTTCTCTG AGTATCCATT TCCTTATCTG CTTATTCAA
C/T
TGACTAGTCA CCTCCTCTCT TTGGATATCT AATAGGTACT TAACATTTAA AATGCCCCAA
ATTGAGCTCC AGATTATCAC CATTCCCCCT

01T156 130bp
TCCTTCTCCC CTGGTGTTGG GGCTTCTATT GTGAGGTGAC CTCTGGCTG CTCCCTTATG
GGTCCCAGGA CCTAACCACA GTTG
A/G
CCAATCATAA TCCATCAGGC CCAGTTTGTT CAAAATGAAT TGCTC

01T157 135bp
AGCATGTTTCG GATTTTCATGA CTCTTGTTGGT TTTGTTTCCTA GACAGGACCT ACCAGGGGAG
CCTCCTGCAA ATGAG
G/A
TGGTCTTCCT TTTCTACTCA TCACATTCTA TGCCTGCCCT CTCTAACCTA CATGGTATA

01T159 139bp
GTTGAGTCAT TTGGCCTCCT TGATCCTCAC GTAAATTGTG GCATTATTAA AGTT
C/T
GGTCTACATC AAATGGTCAT TACAAAAATT CAGTAAGTGT ATAAATATAC TTTTAAACT
AAAAAGCTCT CAGGAGGCTG AAGT

01T160 147bp
CCCCTATGTC CCACAAACCT GCCAATCTCA GATTTCTGTAT CTCAGTTAA GATTCCTTCA G
A/G

Table III

TTTTTAGTTA TTCAGGTTAA ATAATCTTTG ATCTGTATCC TCTATTAAGT CCATCAGAAA
ATCCTGTTGG CCTTTC AAAA TATAT

01T162 136bp
AATTAGGTTT GAAAAGGGAA ATAGTAGAAT TAGAGTTGGG TTTAGAAACA AAATTAGTCT
TGTAATAGTA ACTATGCT
C/T
TTCTAGAGTG AGGCAGTATA GTCATGGAGG AGAACTGCCA AGGGATTATT TTAATGA

01T164 122bp
TTAACTTGTT CACGTTAAGT CCATTCATAT ATTTTGAATA AGGTATAGAG GAGAGTTTTT
GAGTGACTCC TCACTC
G/A
TCTGAAGGTC TGTGACCTAT GAACTGCCTC AAGGCTTTCT CTTCA

01T166 138bp
CACATTTCTT TTCCATGTGG TATGTGGTGA AAAACAGAGA AACAATAAAA CCCAAGAAGT
CTTATTATTA TGACTCCCTT CTTAAATGC C
C/T
AAAGAGCTCA AGAATAGTAT CTTGGGAAAA TTACTATGTG TATGGA

01T167 105bp
ACAAAATTTT AATGCTCTGT GGATCATTAT CTGGCAACAG ACCAACAGCA GA
G/A
CATAAAACAT TAACAACATA AAGCGGGTTC TGAGTCCTTG GAGTTTCTAA TT

01T169 131bp
CATACAACCT CCCAAGACTA AACCAGGAAG ATCAAATTCC TTACTAGACC AATAACA
T/C
GTTCTGAAAC TGAGACAGTA ATTAACAGCC TACCAACCAG AAAAGTCCAG GACCAGATGG
ATTTACAGTC AAA

01T171 133bp
GCAAAGGGTA AGAAGAGGAA GTGGCTTCCC TTAAGTTAGA AGCTGTTTTT ACCTATGGGC TG
T/C
GACAATGCAC TGGCCATGTG TTCTAGACCT AATCTGGGTG AGTGAATAAC TGGGAGGATG
TGGAACCCAG

01T172 148bp
ACACTCCAGG CCTGATACTT CTGGTGTTAA GCAATTTGCA AAATGATATA CTAATGACCT
TTCAAAAAGT TATT
A/G
CCACATCTGC TCTTTGTCAA GTGCAAGAGC CTAGTATATA GAAAATAATA TTAAGCTCCA
AGTGAATACA AGA

01T173 148bp
TTATAGAAGA TCCCCATTGA CGATGCTTTC AAGTTGAAAG AACATTTAGA TAAGCCATTT
GATATAGAAG TGACTTTTAT TTCACGGTCA AAACAATT
G/A
TCAGCCAAAG AAAGTTCCTA ATTTTGTGTA TTTGTGCACC ACAGTAAAT

01T174 140bp
AGACAGTTCA CTGTATTCCT CCCCCAATTC CTAGAAGAGT AGTAAGGGTC TTAAGGCGGG
AGAATGAGAC CTCCTGAAAT
A/G
CTTATGAAGC CTTCCCTTAT CAAGTACTCA CAGCCAAATA TTTCAGAGTG GCGTTAATT

Table III

01T176 147bp
CAGCTGAGGC ATTAATATTC ATTGGATTGG GGGGGTGGTT CCAAGATGGC
T/C
GAATAGGAAC AGCTCCAGTC TACAGCTCCC AGTGTGAGCG ACGCAGAAGA TGGATGATTT
CTGCATTTCC AACTGAGGTA CTGGGTTTCT CTCACT

01T178 134bp
CCTGTTAATA GCCACTACCT TCTTTTCACA TATCACACTT CCGCTTGCTT GTTAACATTC
CTCAGTTTTT ATTTATGG
C/T
TCAATGAGTC TGTTTTGCTT TACTTTATTT TAATTACTAT AGAATGTACT GGTAACTTTC TGATG

01T180 119bp
TACCAGATTT GAGGCTCAAT ATCTACTTCT GAAGCTGGGA GTTGCAATCC
C/T
TGAGTTTACC ATTTTCTTTC ATCACTTTGT CCAGTGAAC TAGGACCAAC CAACCAACTT
TGTTATGT

01T182 139bp
CATGCCTTTG TCAGGAGGCA TTCCCTACGT TCAAGTCTTA AGCATGTGTC CTGTATAAAA
TCAGTCTTTA GCGTCTCCCA AAAGAGCTAT CACTT
CCT
C/T
CTTTTATGAA CTTGCTGTAT CTTGTCTCTT CACTTGAGCA CCT

01T184 129bp
ACCCAGCCTA GGGCATGGCA CGAAGGAAGC ACTCATGGGG CTTGGC
A/G
CATAGTGGGA GCTTGCCAG TGCAGGGCCT GGCTCTTGCG TGCTCAGGAA ATGTTTGCTG
AATGGAATTT CAGTGAATG GA

01T185 134bp
TTCAAATTGT AGATCTCCCC CTCCTATCTT CCACCCATA GCTAAGAAAG GAAACCCAGG
GATAGAACTA ATTGAACCTT ATTAGCCAG
A/G
GGCAATCGAA CCCAGTGCCA ATAGAGAGAT GGAATCCAA TTAG

01t187 145bp
GCTGCAATGG CGTGCTGTGC TTGGGGGCAT GAAGTGTGCA GGGGTAGGTA TGCTGGCCCT
GAGACTTTCC CCCGTGAGAA TTTCATTGCC ACAGC
A/G
CCAGTGGGTG GATCGATAGC TTTAGGAAGG TGAGGTTTCT TTTGTGGAG

01T188 143bp
TAAAGCTGTA ACAGTTAACC TCTTCCACAT GCAGCATCTG CAGGCTGCTT CCCTTGCAGA
CAGTTTACAG TCTCTCTGTG
A/G
TAGTGCCAAA CTCTATGACC CAGGCCAAGA GTACAGTGAA TTTGTCAAGG CCACAAATTC
AA

01T189 140bp
CCAAGATCGT GCCATTGCAC TCCCGCCTGG GCGACAAAGT GAGACCCCAT CTCAAAATAA
GTAAATAAAT AAACA
G/A
AAAAGAATTT CTTAGACGAA ACCTTGTGCC TTTTGTGCTC AGTTGGATAG GAAGTGAGCA
TCTG

Table III

01T192 148bp
 AAACATTTTT AGAGGCCAAG TGTTTCATGTT CATTCTTTAT CCACTACAAT CATATACATC
 AACTTTGAAT GGAGTTGTTT GTGATTTGGC CTCATTA
 A/G
 GCTAAAATGC TTATGAAGAT AGATCTGCGG TTTGAGTAGC TTCAAATTTA

01T194 135bp
 AAGACTTCTG AAGCACCAGT ATCTGAAGAG AAAGCAATGG AACACTGAGG AGAGATA
 C/T
 GAAGAAAGTG GGACCATAGA GGCAGAGAAA ACCATGAATG ACTATGCTTA TACAAGCCAA
 ATGCAACATT TCAAGAA

01T195 132bp
 GTAAAGGGAG TGGCCTGTTC AATATGGGAA AAGACTTGCC ACACATTAAA GCATTTTTC
 A/G
 TCTTATAAAA TTGATGTATT CTTGGAAAGT GTGTAAATTC ATTTTACATG AAGGGAATAA
 TTTCATGTAA AG

01T196 142bp
 TGCAAAATCT TGTATTGCTT GACTACCCAA GTATTAACTG AAATAGTCAT GCCCATCAGA
 CACAGGCAGA GTTTATATAG TGAAACAACT T
 A/G
 AAACAGAGTT TATTAACAGC AAATATTCCT AACTCCATA GCACAGGAGT

01T198 116bp
 TGGCATTATG TGCCTCTTGA TGTGATGCAC TAAAAAGGAT ACATCATAGA GTATTAAGGC
 CAAATATGCA
 C/T
 AGATGAATTT AATCAGGAGA AAGCAATCAC ATAAATTGAG GAAAT

01T200 138bp
 TTTACATGAT GATGACACAA AACTGTAAA GGACCTCTGG GTTACTTGTT TATAAGCTAG
 TATTTCTGA ATCAATTT
 C/T
 TCTGATCCCT AGATATTTGG TAGGTGAAGT CATACTATA TATCCCCACA CCCTAGAAC

01T202 139bp
 CCTTTTCATT TGTCATTGTC TATCACTACA CTGTAAGTAC CACAACAGAT GGAACTTCT
 CTGTTTGTGTT ATTAGT
 A/G
 TATCCTCACA ATATTTGTGA AATGAGTGAG AGACTCAGGA TACAAAGGTG GAATAAAGC
 AG

01T205 107bp
 AGTGGCTTTC AAGATTCTCT TTTTGTCTTT GGATTTCAAC AGTTTAATT
 C/T
 TGATGTGTAT AGGTGTTAAT CTCTTTTGAG TTTATTACTA ATTGCAGTCT ATCTGGC

01T206 121bp
 AGATGCTGAC CACAAGCCTA AAACATGAC CCATGCTTCT GGTAAACAG CTAAAAATTG
 GGGTTCCC
 A/G
 TGGCCCTTC CTCAGTTTTG ATTAATTTGC AAGAGTGGCT CAACAGAGCT CA

01T207 124bp
 TGGCTTATTT TTTTGATATA CAAATTAGAA AGCAATTCAT AAACACAAA AGATCTGAGA
 AGATCTGTAA TTTCTA
 A/G

AGATTAATAT AGTCCGTGTG ATCAGAGGAA TGTCATTGCT CAGCAGT

01T208 120bp
AATCGGAGAG CAGATTCTAG TAGTTTAGCA GAAAGCAAAA TAGAACAGTT AATAATCATT
AACTTAGACT GC
C/T
GAAGGCACCT GAACTTAGAG TAAAGCATGA AGTGCTTGTC TTTGCCA

01T209 127bp
AAGATAATAG CATGATGCTG CTATAAATAA ATGTATAGAT TGATATCTTA AGTGTTCTGG
TGCTGAGTTA CTCA
A/G
AGAGAAACAG ATCTCTAAGT TTCTGGTGAT GAGTCACCAC GTGAGAGAAA TT

01T211 100bp
GTTAAAATGA GCTCAAGATG TGTAGACGTA TTATGTTTTT TTAGGCTA
C/T
TGTTTTTTTG CAACATTTAG CAAATGAATA GGATAGTACA GGGCTTTTTT A

01T213 137bp
ACGCCAGAGG CATGGAACAT TTTCTCCATC ACAGCTCTCA AAAGGAGTCA ACCCTACAGA
CACGTCAATC TCAGACATCC AGC
C/T
TCTAGAACTG TGAGACAATA CATTTCTGCT GTTTAAGCCG TCAAGTCTGT GGC

01T217 134bp
TTAATGAGAA AATGACCCAA TGATAATGTA TATGTAATTA AGATTTTCATT TGCTTCCCTA
TACACC
A/G
TGAGAGTTAA TAAATATAAT CCTCTATGGG CAATTTCTTT AAATCACAAG AATATTGGTC
CCTGAGG

01T220 126bp
AATTTTCTTC ATAACACTGT TCTTCATTAA AAGGTAGCTT TATTTTATAT CTCAGTGATA
AAAAGCCACC AAATCA
A/G
TTCTAGTTTT GTCAACTCTG TTGGTATGAG GAATCTCAAG ATTGAAAAT

01T221 120bp
CCAAAGGAAG TCACATTGTT TTAAGTGTAA AGTACAAGTT CAGAGGTAGA GGTTCCAAAT GC
C/T
TAAATTCTTC ATAGATTAGT CTTGCTGAAG TAAAGAATTT GAATAGGGGA CATAGGC

01T222 140bp
CCTCAGGCCC TCACACACTC ACCTTTCATT ATTCTTGTCT TCTTGACCAT TCTTTATTC
TCATTAAGGC CACC
C/T
CACAAATGAA ACTCACCCTT GAGTTAGGTA AAAACGCTCA TAAGCATAAT TTTATCCCT GTGT

01T223 103bp
TAGGGCATCT TGACATCTGC TTTAGGCACA CTGAAATGTT CAA
C/T
GGCAAGAGTA TTTAGGACTG AGAACATCTG ACCACTCAGA GCAAATTATT TGAATTCT

01T224 141bp
CAAAGCTAAA AGGGGCATCT GAGACAGATT TCCTTTTGTT TTTACTGGCG TGTCAAATGC CAC
G/A

Table III

GTGACAGCAA AGGAATAATC TTCAGTTTGT GTATAATGAG GTCTGAAATT TCCGTCGCCA
CATATTGATC ATGAATC

01T228 132bp
CGCTAAAAAG GGAAAGCCTT CCTTCCTGCC CTAGGACATC CCTGCCAACT T
C/T
AGGGAGGTGG GAACCCAGCT GCGCTCTCTA CAGTATGGGT TACTTTTGTG TCTGGAAGGT
GTCTGACATC CTGAGACCTG

01T230 142bp
TGAATTGTAC CTTTAAAAAT GGTTAAGATA GTAAATTTTA CCATCTTCAC AGTTTCCCGA
GATTGCAAGG CCAGCAGTTA AAGACAAAAA CAA
AACTA
T/C
TTCCAACCTGC CCTACAGTGT GCAGACCTTT CCCTTGTCTT GCCCTGAG

01T231 131bp
TTTTTCAGCAG TGATATTCCT TGCTATGTGT CATTCTATTT GTATGGAACG GCCAAAAGAG G
T/C
GAAGCCATAG AGACAGAAAG TAGATTTGTG GTTGCCAGGG GCTGTGGGGA GGGGCCTGGG
GAGAGATTG

01T232 142bp
ACCATGAAAA TAGATGACAG AGTAGGCACA GGAAGACCAG TTAGGCCCAT ACAGCAATCA
AGGTAAGAGA TGATAGTGGC CTGGAACA
A/G
CACGTAGCCA TATAGGTGAC TATATTTATA TTTTGAGGGT GATCCAAAAG GAT

01T233 113bp
GGAGGTTGGA GGGCAGGGGC AGATAGGCCC TACCTTTCCA TAGGGTGAGT GGCAAAGAAT TTG
T/C
AGCTATCTTT CACAACAGCT TGGTTAAGCA AAATTTTTTT TTACCATTT

01T234 130bp
GGCTATGCTA CAGTCTCTAG CTAAATGGAA GACACATTCA TCCTTCTCC
C/T
TCTGACTGCT TTGATCATCA TTTATTGCAT CTCATAACTA ATTTTCTAAA GTTTGGATTG
GGACTTTTCA GGTCTTTTTT

01T236 128bp
TTCTCTGGGG GAACCTGTCT CAGTGTTGAC TGCATTGTTG TAGTCTTC
C/T
CAAAGTTTGC CCTATTTTTA AATTCATTAT TTTTGTGACA GTAATTTTGG TACTTGGAAG
AGTTCAGATG CCCATCTTC

01T237 141bp
AAAAGGCTAT GGAGGTCCAA CAAAGAACAT CCCAGCTCAG CAAAATGAGT GGCAGCTTCA
GGTGCGAAGT GGCTCTGATC TAGGCGTTGA GGC
C/T
GAGTGGGATT TGGAAGTGTG GAAGTTGTGG GGAGGAGGCA TATTGCA

01T240 121bp
GGCTGAAAGG ATGAGTGATT TTAAGGGGAA GATTTCCTCA TACTAGCTAG AACCTCTC
G/A
TCACGTCTGG CCCCTGTGAG CCTCTGAATG TGTGCTCCCT GGCTGAGCAG CTGATACACC
CA

01T241 107bp

Table III

TGCTCTTATG TGCCTTTTTTC ACCTCAACAT GCAATGGGAT AATTAAA
 A/G
 AGGGTAGATT TTTTTTTATG AAATAGCATT TTAGATGAGG TAATAGAGGA ATACAGATG

 01T242 141bp
 ATTTGATCCA TTCATTGCTA AAGCAGTAAT TTTGAACCAT ACCATTGCTA AGTACTTAGT
 CATCAATATA GGGTTGAATA GTTCATCTGA CA
 T/C
 TTTTGTTTTA ATTACTAAAA TGTTTTTTTG CCCAGTTCOA TTGGACCA

 01T244 119bp
 TGGAAGGGAC TGTCTCCCT GCCTGCAGAA TCTGCTGTGG TATCTCTTG
 A/G
 ATGAGGCCAT GCAGCCCCCA CCTGGCTCCA CGTTCATTCT TGTCTGATC CTCAAGCACT
 CAGGGCCTC

 01T246 99bp
 CTTCCCTTCC CCATTTAGGA CTCTGACGCA GTACAGTTAA TCTGTGCA
 C/T
 AGGAAAGAAG AGCTGTTTGA AGAGGTTATT CGGTAAATGC AGAGAATGTC

 01T247 143bp
 AAAGAAATGA AAATGAAAA ACAGTAAATG AGGGAAAGGG AAAATAATGA TGGCAAGGTA
 AGGAGGAG
 C/T
 TAGAAGGTTA TGCAAACTA GAGTTATGCA AAAGTAGGAG CTAGAAGGTT ATGCTAGAGG
 TTATGCAAAA CTCA

 01T248 120bp
 GTTCGTGGAA GCTCACTGGT AGGTGAAGAT GCTTTCTGAG TGATAACATA TGAGCTATTG
 CAAACATGGT
 C/T
 GGGGATTCCA CATGCCATTT AGCAATAACT TGGGGATAAT GTGGTACGT

 01T249 149bp
 TGGCTCTACT TTCAAAGTT CTTAATTTTA ATATAGTCAA AACTATTTTT TCTTTGGTGG TAAAT
 A/G
 CTTTTCATGT CTTTAAAAA ATCTTCCCTT TCTCTAAGGT TTGAAGGATA CTAGCTTAAC
 TTCTTCCACA GGTTTCAGAA TTT

 01T250 136bp
 ATACCATTCT ATCAAAGAAC GGCATTTGCT TTTTGTTACA CAAATTATTT CA
 A/G
 TGTTTAAGGA CAAAATGAAA CAAAACAGGA AAACCAAATT AACAAGAAAA AATTCCCTCT
 ACAACCTTAC CCCTGCCCCG CCC

 01T251 109bp
 AAAGTGATTG TCAATATGGC AAAAAAGTTG GAGAGTGAAG TGTTTCAGTA TATGGATCTT G
 G/A
 AGAAATTCAA GAGCTAATAG AACTACGCA GGAGACAACT TGCTGGA

 01T253 141bp
 TCTCCAGAA TTCCCAACAA CCAAGGTTG CATTAAATTAC TTTAATGGC AAAACCACTG
 TTAATTTTGC ACCAA
 C/T
 CTAATATTAA CCTATTGTGG GAGGGACCCA TGGGGAGGTA ATTGAATCAT GGGGCCAGTC
 TTTC

Table III

01T255 139bp
 TCCTAAACTG AGTGTATGCA GTAGGTGGTC AACAAATATTC ATTAGTA
 A/G
 ATTCTTTGTA TTCTTCCTGA GGGCAAACT GCTAAACTC CCTGGAGAAA AAGGCAATAC
 CTGGCAAACA TAAGGCATCT CTCCAGGCTT A

01T256 139bp
 CTTTGTGTTA ATGGCTGAAC AACTGTACAT ATCTGTAAAA CTCATTAAAG TATATATTTA
 AAATGGGTGA ATTTTAATGT AGGTAAATTG TACCTCA
 A/G
 TAAAGATGAA TTTTTTTTTT AGCTGAGCGG GTGCAGAAAC AGTAAGGAAT T

01T257 114bp
 CTACTGTAGC AGAAAGCCAA TAGAAAATGT CTAAATTTTA TCACTAGGAA GCAGCAATAT
 A/G
 AGCATATTAT TTAGGAATAT AATAAGACAT CTCGAAGAGT TGACAGTGGT TGT

01T258 115bp
 CACTAAGAGG TAAGGCAGCT CAAAGGGCGT TGGCTAATGA AGTGGATTAT TGGGAGGG
 A/G
 TTTACTCTTA CGGGTTTTAG TGGGGGAATA CATTAGGTAA GATGTCTGCT GGGAAAT

01T259 137bp
 TCAACTTGGT GACTTATATA TGGAGAATTT CAAATATGTT CTAAGTGTTT GCCTATATAT
 TTTTGGTCTG ACATGGGGA
 A/G
 AGAAGGTTTC TAGGGGAGAC TAATCTCTGA GCACTTACCA GGAGAGGACA CCTAAGG

01T262 139bp
 AGAGGCACTT TCCACCTGGT TACCAACCAG AGTGGTAAGT GGCCATTGAA C
 A/G
 CTTTGGATAA CTTATTAATG GATGTATATG TGTTATTCTG CCTCTTCAAA ACCAGAGGAG
 GGCTATGCTG TAATGGGCTT AGATCTA

01T266 149bp
 GCCCTGAGAC TGTCTGCTAA TTTGGATTCT AGAACACAC AATCCACCTT ACAAGTA
 C/T
 GTAAGGAGGA AAGTAAATAA CAAACGGGTA AAGTGCTTTG TAAACTGTCT ATACAAATAT
 AAGAGACCGT TATTACAACA CAGCGGAAGA A

01T267 97bp
 TAGAACACAC TGCCCGCAAT ACCCCCCCTT TCTTGCTGCG CCCTGC
 A/G
 GCTCCCGCGT GGAACCTCAT TCTTCCATTT GCCCCCGCC CCCAGTTGCT

01T268 108bp
 CTTGTGGTGA TGGATATCCT AAATACCCTG ACTTGATCAC TGCACATTCT ATGCATGTAA CAAA
 T/C
 ACTCACAGGT ATCCCATAAA TATGTACAAA CTTTATCAAT AAAACATTTT TTAAAAAGAT
 GTGCTTCTGA TCA

01T270 132bp
 GGGGACTGTG CCTTGCACAC CGGCCGCGAC CTAGCCCTCT GCCCCCACT CAGTACTTCC
 ATTAGTCCC GTGGAA
 C/T
 AGGAGAGACC TGTTCCCAAT CTGGCCAGA AACTAGGGAT GGGGGGACTG TATTG

01T271 149bp
ATTGAAGAAG AAAAAAGAAC AAAGTATTTT TTCCCCATGT TTTCCTGGTG TCTTTTTTCAA
AGGTTTGTGT CTTAACAGGT GCCAAGAGCC TGCAATC
C/T
TTCCCAAACA GCCCTTTGTT CTGTGCTCAA GTCAACCCAC TGGGACTTTA C
01T272 124bp
CTGACTCCTT TCCCTCAACA TGCAAGCATG ATCAAGCCTT TCCCATTTTA AAGTAAT
C/T
TTCCAACCTTA CCTCTCCTTT CATCATCCTC TCTCTTTGGC CTTACCATCT TAGCGAAATT
TATTGA

01T273 149bp
CCCAGAAACC TTAAATATAG ACAGACTTTA TTAATTTATG TAGGAAGCCA AAAATAGGAA
ATAAAAAGAT C
C/T
GGAGTTCAGA TATACTGATA TATTCAGCAA CTGAAACTTA CAATTCCTTC AATTCAGTCA
GAGCAGAGAC ATTTAAA

01T274 145bp
CAAACCTTGAA GGACTCATTC TGAGGCAGAG AATGAATAAA TC
A/G
TTACCTTTGT GAAGCATCAG AATCAGCAGC ACTTTCCTGT CCCAGGAGAA GAGGGAAGGG
GAGGATGGCA CGTTTCAGGG CTTAGGGGAG GATAGGGGAG AA

01T277 105bp
CGCAAGCCCA GAAAGACGGC TGGGGGCAGG GGTGCTGCGT ACTGTTCAAT GAGAGCCATA A
T/C
GTGGCTGTAA CTGTCTTCCT CATATTGCAA GAACACTGCT GGC

01T278 124bp
GGTGAATCAG GAAGATTTCT AAAGTCCTAG TTCTACAACT AAAGCATTAG ACGATTAAGG AAG
C/T
CCTTGATATT CTCTCAGAAC TTTCAGTGAC CTTCTGCCCTC CTACAGACTT CGAGGAAGAG

01t279 142bp
GCTTGCCTGT GCTGCTCCCT CTGCCCACTA GAGGGAAGCC CAACCTCAGG CTGAGGCCTA
GAAGGGGA
C/T
GGCTGCGCCA TGTGGGGCAG GGACAAGGAG GGGAGGAGAT GGCCTGCCAC TTCCAGACCC
CAGTGCGAAA ACC

01T281 149bp
ACCATCAGAT CTCATGAGAC TCATTACTAT TACAAGAAAA ACATGGAGGA AACTGCCTCT
ATGATTCAAT TACCTCCACC TGGTCC
C/T
ACCCTTGACA CACAGGGATT ACGGGGATTA CAATTCAAGA TAGATTTTGA GTAGGGACAC
AG

01T282 145bp
AGGACTGCCA TTTTCTAATT CAGCAAGAAG TCAAGAAGTA TAGGATAGGT GTGAAGGATG G
C/T
GAGATCTGTA AATGTGTAAG CTTCATAACT TCTCTGTGAC TTGCTTAGCT TTATTCTGTT
TTTTTTTTTG TTGGCAAAC GTA

01T283 137bp

Table III

AGCCGGTTGG TCTGGGCAGG AACGAAGTCT GTGTGGTCAA AGGGGACCCG CGCCGGCGAG
 ACTGGGATGC TG
 C/T
 TTGGGCTGGG CGGTCAGAGT ATGGAGTGGG GCTGGGGTGA GGTGGCAAGC ACCCCAGGGT
 GGGA

01T285 149bp
 GTAGAACCAT GAACCAATTA AACCTTTTTT AAAATAAATT ACCCAGGTAT TTCTTTATAG
 CAGTGCAAGA ACAGACTACT AATACACCTA GAGACCCA
 C/T
 GGGACACCAT CAAGCAGACC AATAGATACA TAATGACGTT CTAGAAGGAG

01T286 110bp
 GGTTTTATGC ATTTCTCTCA AACACCGACT GCTCTTCACG CACTTTCAAA CCATATT
 T/C
 CCTGTTCTCG CAATCCACTA TAGTGATCTG ATACATTAGA AAGCTGCCCT AG

01T287 122bp
 GGTTACCAGA GTTCCAATTC AATTAACACA ACTAACTGAC TATTGTAACT TGTAGACATT
 ACCAATGGGA ATTAAC
 A/G
 CTTCTGAAAA AGGTTTATTT CTTCTCTTGA AGAAGAGATT GGGAGGAAAG GTATA

01T288 121bp
 GTTGAGCATT TCAAGATCTT TCTCAGTAAT AAAATAAGTA AAGTATTTTA AAAATAGAAG TT
 C/T
 TCAATAATCA ACAATTGAT CTCTGTTGATA TCTATAGAAT GCTCTAATTA ACGGAGAA

01T290 125bp
 GTATGCTCAT TAAACATTA TTCGTTATAG AAAAAAAGTC TCATAAAATC TGGAAGCAAA
 TGAATGTCA
 A/G
 TTAAGAGATT ATTTTTATCG AATGGAAATA TGAATCAGCT TAAATTGTGC ATTTC

01T291 146bp
 CCCAATCTAA ATGTACATCA ACTGGTAAAT GAATAAAAAC ATGTAGTACA TCTATACAAT
 GGAATATTAT TCAGCAATA
 A/G
 TAAGGAATGA AACACAGATA CAAGCTTGCA CTTTTATAAA CCTCGAACAT TATGTTGCAT
 GAAGAA

01T292 121bp
 ACTATTCTGT TCTAAGGTTG CACTCCAGGT TGAAATTGGC TGACAAGGT
 T/C
 TTAGCTTGGG TAGGATTTAT TCCCATATA TTAAATTATT TTTTAAATTA GTTCAATGCC
 CAGGTCATTT-C

01T295 116bp
 CTATGTCTGT CCCTTGCCCA TTTACCCGCT ATATTCTGTC TATATTTTC
 A/G
 CTGAATTTGG GTCCTGCTTC TTATGCTTTA TGACAATGTG TGGTACAGCC CTTTGAATCA
 CTGTTT

01T296 143bp
 ACCTGAAAGA AAGGAAATCA GTATATGGAA GGAATACCTG CACTCCCATG TTCATTGCAG
 CACTATTAC AATAGTCAAG ATACAGAATC A
 A/G

Table III

CCGAAGTGCC CATCAGTGGA TGAATGCATA AAGAAATATG GTACATGTGC A

01T298 117bp

TTTCTGGTTG CAGCACTAAA AGTCAACTTG CCTTTTGTTG GCCTGC

A/G

TTGACCATTT TCTTCACCAA CTAAACACTT TCAACAGAAT AGATAAACTT GAATCCTAGA
TGAGATAGCA

01T299 142bp

ACATAATACA GCTGCCACAG CCCTATGTCA TTAAGCAGTT GAATTAATCA ACCACTTTGC
TACCCACCTC TGAACTTTTT GCTTTTGAG ATAA

C/T

CCCCTTTTTG TTTAACCTAT TTTGTGTTGA ATCCTTACTT ACTCAA

01T300 124bp

TCAGTGACCC ACAATCCATT CCTAAAAGGG AGAGCCTCCT GTCTTTCTCT CAGTTCCTC A

A/G

GCTCTTAGCA GGACTCAATA AGAGCCCCAG AAATTTCCCA GAAGTAGGTG ATTTAAAAAC
AC

01T301 124bp

TAGAGTAAAT GTGGTCTGCA CAGGTGTAGG AAAGAGTGTG GGAGAGGAGG AGGGGACAA

C/T

CTCATGCCTT TCTTTATTAA AAACACATAA AATAAACCTT ATAAAATGAA AAAGTTCCAT
GGAT

01T302 103bp

GGAGCATTTT TTGGTATCTT TATTTTTTAG ACCACATCCT TCATGGTTGC AT

G/A

TTGTTCTATT TTCTTAGGAA TGCCTGAAG CTTGGCTTTG CTTTATGTT

01T303 90bp

AGGATGCAAC AGGAGCGGGG TTGCCTGATA AGACAGCGAT AGAAAACC

A/G

AGAGATAAAG GAAGTCTGGC CAGCAGCAGC TAGTCTAGAG G

01T305 106bp

GAAGGGTGTG TGCAAGTGTA GAACAAATTC CTTCCGTGAT TAGTCAAGCT ACCTGACTT

T/C

AAACAAGTTT TATTTTTGTC TCTATTACTG TTAAACTGCA TGGCCT

01T306 115bp

AGGCTGAAAT GGTGTCTATG GATTCCAGAG GCCAAAAGGC TGGTGTGGAG TCA

C/T

GGCAACTTTC CTACCACTAC ATTCCCCCTT CCTATGAGTT TCATCGTACC AATGATGGCT
G

01T307 115bp

ACAACTGTGA ATTGTGGCCA AGTCTCCCAA ACTGGTTTTG TTCAGTTCTG AAACTTGCAA

C/T

ACACCAGAAA TTTTAGGGTT TGGAAATTAG GAGATCAAGA GTTTGAATGA AGAA

01T308 115bp

CAGACCAAAA TACATTTATG ACACCTGTGA AAGTAGAGGA AGAAGAAAGG TTTGTGTAGG
AAGAGTCTCA GA

C/T

CAAAAATCAC TTCTATGAAA GTTTCAGCCA GGGCCAATGG TG

Table III

01T309 131bp
 AAGAAGCCTC CAGGAAAACA CATCGCTTGC TCCAGGAGTG TGTTCCCAGA GTGTCGACAC
 AGCTCCAGC
 A/G
 TTTCTCACAG CCTCTGCTGC CAGGAAAGGA TAAACACCA CCCATATTCA GGAACAAAGA
 C

01T310 135bp
 GCCCACCTTA ATGACCTCAT CTTAACTTGA TAATCTGAAA GCACCCTATT TCCAAATAAG
 GTGACATTCA
 G/A
 AGGGTGTAG GACTTCAATA TCTTTTGAGG GGACACAGTT CAACCCATAA CACCTACCAA
 CGGT

01T312 145bp
 GACACTCTGT TGAGATGGGG GTTAGACATC TAGGTACTGT TCCTGTTTCA CTACT
 A/G
 ACTAGCTACA CAATTGTGAG CACATTGCTT CTTTATCTGT TTCTCTAAGT CCTTCTTCAT
 CAAAATAAT TGAATTTCCA TTTTGCTGG

01T313 134bp
 CAAAAGAAGG AACAGGGAAT ATACCTAGAC TTTAACCTTG TT
 A/G
 ATACTATAGT ACCTGTCCTG AGTAGTACAT TGTAGAGGCC AGCCTGACTA ACTGGAAGTC
 AAAGGAGAAA TACCAAGAAG AGGAATGGCC T

01T314 110bp
 AGGGGAGAGT TTCTTTTTTAA GTTATTATTT CATATTTTCA GGATTTTCA TG TCTTCCTCTG
 TCATTT
 C/T
 CTCCAAGCTC AGTTTGGGGA ACCAGCAGTC TGTGTTAGTT CAC

01T316 143bp
 ATCAGGCTCT ATTAAATGGT GGTAGGATAT GAGGCTACAG ATAACAGCAA AAAAATTAAT
 CAAAGTTTCA ATTA
 A/G
 CACAGTACAC ACAGATCAAC CCACCAGCTA TTATGTATTA GTTTTAAGCA CTTGTCATTA
 TGCCTCAT

01T317 146bp
 TGGAATACAC AAATTTTGGG AATAAAAGGT TCAAGTTCCA ACATGCCAAA ATT
 C/T
 TACTGAAAGT AACAACTATA TTAAAGCTTG TAGTGACCAG GTACAGTAGC TCATGCCTGT
 AATCCCAGCA CTTTGGGAGG CTGAGGCGGA TA

01T319 136bp
 GTTTACAAAT GAACTCCTTT TCTGTCTTTG CATTTTAGAG AAATAAGTG ACTAAGGAGG
 AATGTCAAGG ATCATAGTGA CAA
 C/T
 ATGTTCTTCA AACGAAGCTA GGAGACTGAG AGGGAAGTGA TGGAGGGCTG AC

01T320 145bp
 TTTGGCTCCT CTATGGGCAC AGCTGGCTCA GAGGGCTCTG AGCAGCATCT TTCTATTCTG
 GGAAACTACA GCCAC
 G/A
 CGCCCGTGTG AGCAAGTTTG CACCATCACG CTCTGAGACC AGAGTCCTGC CCTTTCTCCT
 CCTCTGTGC

Table III

01T321 133bp
 GCACTTGTTA GAAACACGAA ACTCGTGGGC CTGACTTCAG ACCTACTGAA TCAGAAATAC
 TGGATGGGGC TCAGCAATTT G
 T/C
 TTTTAACAAG CTCTTAGCTG ATTCAGATGA ATGCAAATGA CTCTTAACCA C

01T322 141bp
 TCTTTTGATC AAAGCAATTT TTACTTAGAA GGAAACAGCT GACTTACAAA GAAATTGCAC TGAG
 A/G
 CTATTTCTAA ATAAAAGTGT TTTTGCTGTG GCATTGCAGG GAATTGAGGC ACCTTCCATA
 CTGGTGGTTA CTTACA

01T323 118bp
 AGTTTTCTAC AGAAATCACT CAATGAGCAT TGATGGCCTG AAATGAATTT
 C/T
 GGCTTAAATG GTACAAATGT TCAGAAGCAG GAAAGCTCAG GGCAGGTTTG AGGAAATTAA
 GCAGTCC

01T324 129bp
 CAGTTGAAGC CACTACAACA TCTAATACAT CAGCCTTGGA AGCCATCTTG CAGATCATCT CATC
 A/G
 TGGGAAAACA CACAATATCG ATGAAGCAAG CGATAATGCT CCACACACTG TCGGCCTAAT
 GGCA

01T326 133bp
 GCATAACCCC AAAGGGTATT CTTAGGATTT GTAGGTAAGG GTTTGAGAAG
 A/G
 AATATGTCGG CTTAAATATG GAGAGAACT TTTAAATGCA GTCAATAGAT ATGATGGACT
 GCATTAAAAAT ATGTTGAATT CC

01T327 132bp
 TGTGCTTTGG TTTCTTCTCA GACTGAAAGC TGGACTAGGG AGACAAGTGC TAGAAAATGA A
 A/G
 CATAAAGCAT GAAGGGTATT TTTTTTCTCC GTTAAAAGAA CATTACACG GTCCCTAGTG
 TCTACAAAAG

01T328 146bp
 GTGTGTCTCT GACCTGGGCT CTGATAATAG GACCCAAAAT CCCATCTTCT TTC
 A/G
 TATTGGGATT CACTGTATGT TTGGTGAAGG ACTCATCTTC GTACTGTGTG TACATAACTT
 TCTTATAATG TTTTCCAATT TGGTTTGAGA AA

01T330 111bp
 AGTGACAACT TAGACATTTG GTGAAAACCTC ATTTTCATTT TATATG
 A/G
 TAGCAGCAGG TTGTGCAGGA CATGAAGGCT ATACAGTTTT GTGAGGCCTC CTTAAGTAAA
 AAGT

01T331 136bp
 ACCACTCACT CTTTGGGTCC GTGCCATCTT TAAGAGCTGT AACACTCACC GC
 A/G
 AAGGTCCATG GTTCCATTCT TAAAGTCAGT GAGACCACTA ACCCACTGGC AGGAACGAAC
 TCCAGACACA AGATGATGGA AGC

01T335 139bp

Table III

CAGCTTCCAG AGACAGGCTT TTGATCACCA CAGGGTCCTT CCCTTTGTCC CAGTTATCCC
AGGGAAAGCT ACTAATCTGG TTCAGGTGG

A/G

CGTGGGCAGG GGCTGCTAGG CCTGCAAGAA GCAAGCCCAG GACAATCAG

01T336 134bp

AAGTTGAATT TAACAAGCCT TCTATTAGAC TTGAATGCCT GCATTATGAT AATTATAAGC
ACACCTTTCA CCAGT

G/A

TAATATTTTT CCTCTTAGGA GCTGTATGGC AAAAAGAAGT TTTGTGAAAT TTTATTGC

01T340 127bp

CCATTCTAAC TGGTGTGAGG TGGTATCTCA TTGTGGTTTT GATTTGCATT TCTCTGATGG
CCAGTGATGA TGAGCATT

T/C

TTCATGTGTT TTTTGGCTGC ATAAATGTCT TCTTTTGAGA AGTGTCT

01T341 108bp

GAAGCTGAGG GAGCCCTGGG GCGTGGGAA ACAGCGCTGA CAGTTAGAC

C/T

GTAAGAGCCC AGGGTAGGAA CTGGGCCTTT CGCTCAGTAC CTTGGGCCAG GTCTGGCA

01T342 149bp

TTGGAGGTAT CATCTTGACT TCTCTTCTGG TCATGGCTTG TTACAGATTT GGCACCTTTC
ACTTGAC

C/T

TGAAAGGAAA CAGATTTTAA AATTACATTT AATTAGTTG CAATATGAAA CAAAATGAAG
CCAGTTTTTA AGACAATAAG A

01T343 109bp

AGTTTCAGAG TTCAGCTTCA AAGCTAAATG TAATCCCCCG TCTC

C/T

CCTTCCCCTA CAATAGTAAA ATGAAGAAAG CTATTTATTT CCAA

01T344 113bp

TTTTGAAACA TGCAGCGCAA AAACCTCAAAT TTCATAGATT GACTTTGTTC TTAACAGAAA
ATCTCT

A/G

TGAAAGGAAA TTTGTGAAGT AGCAAGAGAA AAAGAAAAGC ATGGTG

01T346 132bp

ATTAACATGG AAGGGGAAAT ATGATAGATA TATAAGGACC CTCCTCCCTC A

T/C

TTATATTCTA TTAAATCCTA TCCTCAACTC TTGCCCTGCT CTCCGCTCCA CCCCCTGCCA
ACTACTCAGT CCCACCCAAC

01T349 126bp

GTGATCCTTT CAAAAATGGA TTCAGAAATC ATGTCACTGC TCTGCCCAA GTTCCC

A/G

AATGACTTCC CAGTCACTCA GAGCACAAAGC TGACGCTCGA CACATCTGGG CCCCCTAAGA
TTTTCATTT

01T351

ATTCCAAAGTTTTAAATTTTCCCATTCGTGTCATAGTTTGGGTACCCTACTCCTCAGACC
CGGGGCGAGCCTTCGGCTGTGACTCAGCACATAAAAAACCAGAACGCCGGAAGTATTTTC
CTACACCCGCCGGATG

A/G

ACGCTGCTCCCGAGCGCCGCAAATACTAATTGGCTCTTCTCTACCCTACAGTCGGCCCCGA
CAGTGGTGGGGTTTCATCCTCAAGCCCTAAGAAAGTGCTAAAAAGACCAGTCTGGATGTG

01T353 110bp
AAATTGTCTT GGAGAAGCCC TCAGAAGAAT AGGGATAGTC TGTTTGAGCG TGTTGTCAAC C
C/T
TCAGTCCTCT CTTGTGATCC TAGTTAACCT TCCCTGGTTG ATAAGATTC

01T354 102bp
CTCTCCTCAG GCCTGACTGG CTATGTATTT TCATAAGTGA AGAATTT
C/T
CTGGTGAATT CATGCGATGC GTTCATCAGA GAATAAGAAA CGCAAACCAT ACTG

01T355 142bp
AGGTCTCATC TTCTTCATGG ATACAGTAAT GCTAATAGAA CCCTCCTATT CCATAGTGT
C/T
GGCTGCTGTG AAGGAGAAAAG GCAATACATG GGCTACATAT TACATAATAC TATGTAAGTA
TTAGCCTTAT CATTATGGGG GC

01T359 113bp
TGTAGGTCAC TCTATCTCTT CAAATACCCT TTAGTGGTAT TTAAGGTTTT TGCAG
A/G
GTCTGGGGAC TTAGGTGTTT CAACTATCAC CATGGATTTC CAGATTTTGT AAAAGGT

01T361 123bp
GAACAGATGG TAGCCTGTGG TGAAGGTTCT CTTTCAGATC TTTAGTCTCT TTTCC
C/T
GTGAATTAAT CTTACCTAGA TCTGGCCAAG AGGAGCCTCA GAGTAAGCCT ATTTGCATCT
GTTATTT

01T362 117bp
TTTCATTAC TTTCTCTGTG CTTAACAAGG CAAAGGGATT ACTGTGCT
G/A
GGGTTACTGC TATACCAAAC TGTCATCTCA GTTCTTCTTG GATACAGTCA GTTTAATTAT
GCCTGGTT

01T363 141bp
AAAACATTCT GCCAGTTATG GTCAGGGAAC TGCATATTTT TAGCTTATCT TCTTCATTGT AAA
C/T
TCTCTAACAC CTAGAACTCT ACCTACCCAT AGTGGACACT CAAAAATAAT TTGCTGAATG
AATAGTAAAT GTGGACA

01T364 135bp
GCGCAGGGAA TACACAAGGC TTAATCCACT AACAGAATAG GTTGAAAATA C
T/C
GAGATTCACC CTCCACCCCA ACAATGCAAG GAGACTCAA GAAATTAATG ATCACAGGCT
GGGTTTGTGA TGAAAGGAAA ACAA

01T366 129bp
GCTGCAGGGC TCTGCTGCTG GTCACCCACG CTGCAAAACC CAAACCT
C/T
CCTCTACTGG GCCCTCAGTT TGCACACATA AGGAAACCCA TTGCCTTCCT TTAATCAGAC
TAGGGCTCTA ACCTAGTGAA C

01T367 147bp
GAAC TTGGAA ATTGATTTGC ATCTAGTAGC AGACAGGGGC TCCCAACCTG AGCACAAC
A/G

Table III

TACCAGGGGA ACTGTGGCAA GAGGCTGTTC TCACAGTCTC TTCCTTGGC TGAGGGATAG
GCCTAAAAAG ATGGAGTAAA CGACTCCA

01T371 122bp
TCATATATGC ACATTGCATC CTAACCACAC CAGACTTTCA AGAGCCTTTG CCTTTGTTTT
TCAGAT
C/T
TTAAACTAAA TCTTATCTAA CACCACCCCA TCCAGGACCA TTTTGTTTTG TTTTT

01T372 114bp
AAAATGTCTG TAAATTACAG CATCTATAGA CAGCTATGTT TGCAACATCC CTTTAACCAC
G/A
CTATGATATT TGCTAACCAT GCTAGTGCTA TTTGTTCTTA TTACAGACCC AGA

01T373 125bp
TGTAACATCT AATTTGTGGC ATTGAGTAAA GTTTAAGACT TGTCAGACCT GCCTTGG
A/G
AGGGATAGCT TCCCCACCCC TTCCCCAGCC ACAAATGGAA TACTGCATTC CACAGTGAGA
ATGTGGC

01T375 104bp
CTCCTCCATC CACTTAAGGT AATCACAGCA CTGTAAGGGG CTATATCAAA ATTC
G/A
GCATCAGCAA CATAAATTTG GTTGACAACT GAGCTGAATA GAGGACCTA

01T376 128bp
GCCATAGACC TCTGCAAGCA AAGCGACCCC AAGCATTTCT TTCTGCCTGA ATAATTA
C/T
GGTTCAGTTC ATCTGTGATG AGAGATATCA GCCCTGCCAC AGCTAATTAC TATAGGAATT
GGCCTTCAGT

01T377 131bp
CTGAAAAAGG TCTCTCTGGC AACAAAGGCAA CAAGGTGGAC ACTGGAATGT GAAGGTGCTA
GAAGAC
C/T
ACAGAAAGTG TATTTAGAAG AATGGCAGCA GCCTGGAAAA GCAAGGATGG GGAATGAACC CAAG

01T380 127bp
CCATGAGGCA GATAAGGGAG TATTTACAGA GGTAGGTAC ACTGGACCTA CCT
C/T
ACGGGCTTGT TATAAGGTTT GGTAACATTG AGAAGCTACT AGGCATCACT GCACTATATG
CATTCCATAT GCC

01T381 126bp
TGAGAATTCT GGCAAGATTT TATTTGATGA AAGTATTCCA TGGTAGTAGA ATACTATG
C/T
GGCCATAAAA AAGAATGAGA TCGTGTCTTT TGCAGGGGCA CAGATGAAGC TGGAAGCCAT
CATCCTC

01T382 135bp
ATCATCATTC AGCATGGATA TTATCATCGA AATTTAAGAA AAGGTATG
C/T
TATGTATTTT AATGGCCTCT AGTGATTCTC CCAGTCCTAA GATTCTATCA TAATTTTAAG
TAAAGAATAT GCCGCATGCA TAATTT

01T383 113bp
CTAACACTTT CCTCTTCATG GGGATAACCA TATCTGAAGA ATGTTTAC

Table III

A/G

TAAGTGCATA ATCGATGCTT CCTGGACCCT CAGCCCAACT TTAGATCTCT GGGGGATGGC
TTTA

01T387 149bp

TGTTGAGGAG ATGGGCACCT AATTGAATGC TTAAAAGGAT ATTTTTCCTA AGCTTTTCTT
GAAGCTTAGT AT

C/T

ACTTCTTAAT CACTGTACTT GACAAGTCAA CCTTTTAATC GGAGCCTGAT AAATCCATAA
CATAAAAAAT TGCATT

01T388 140bp

CTCCCAGTAG GACAAGGGAA AGAATAAAAT ATCTTATCTC CCTGTAGTGA GAC

A/G

GCTTTATTAA GATTTGACAG TAGTTATTTA ACAGCAATAA TTGAGTTTTA TGCAAGATTA
TACACGTTCT CCTAATCTGG CATCAA

01T389 149bp

CCAAACCTGC AGAGAACCTA TTGGTCATTA GCGATGAGAA TGAAGTCAAG TGTTTATTAC
TGATTCACAT ATAATAAAGG TGAATAACAG GGTG

G/A

CTCATAACCC AACAACTCTG TCTCCTCAAC CTGGAAGTCT ACGCCTTATC AGAG

01T390 124bp

CCAAGGGTAT TAGTCAGCTC AGGCTGCCAT AGAAAGATAC CATAGGTTGG GTGG

C/T

TTAACACAG ACTTTTATTT TCTCAATATT CTGGAGGCCA AAAGTCAAAG ATCGATGTGC
TCACAGAGT

01T391 148bp

ACAATCACAA GGTCCCACAA TAAGCTGTCT GCAAGCTGAG GAGCAAGGAG AACCAGTCTG
AGGAGCAAGG AGAACTCAGG AA

T/C

TTGGAGTCTG TTGTTTGAGG GCAGGAAGTA CCCGGCATGG GAGAAAGATG TACACCAAGA
GGCTA

01T393 141bp

CCCTATGATG TTCCCTCTCT CCCCTCAATG ACTGTAGCTC TCTAGTTCTC TTTCTACTAC
ACATTCA

C/T

CACTTAATAT TTTGTACTGC TTTCTTAACT GACAATAAAT GCTGGCCAAT GCTTTCCCTG
TTTGTGCACA ATA

01T394 137bp

TTCTTTAAAT CAAGCACAGG GCAACATTGA ATACATTTTC CTACTTTATA TAGCATTTCT
GCAAGTGCTG GGGTTACATT TTAGTCTTCA

C/T

AGAATGCGTG ATTCAAAAGT TTATTTTTTTT GATTAAAGA CACGAA

01T395 117bp

GATTTTTGGA TATGGTGAAA CATAGAGGTC TAGTTTCATT CTTCTGCATA TGAAAATCCA
GTTTTCTAG AAC

T/C

GTTAATTGAA GAGACTGTCT TTTCCACAAC ATCCCTTTGT CAA

01T396 133bp

GGCTGAAATT TCACTTCCTC AAAAGAACAT TTTCTTGACC TCTAACA

Table III

C/T

TCTAAATCCC ACCCACTCCC TGCTTCATGT ATCTCTTTTC TGTAGCACTT GCCATAGTGT
AGGTTTACCA TGAATTAGTG TGATT

01T397 145bp

CCCTGATATC AGCTAGGGGT CATATGGATA CTGGCTTGCC C

A/G

TGTGCTAGAA CTGGGCACTG GGATGAAGGA ATTACTTCAA CATGTGTTTG GATAGTTCTA
CCCACCTTTT GCAAGGAGGT TGGTTTGTGC GTCTGCAACG ACC

01T398 149bp

GTCCCCACAC TGGGCTTCTG GACAGGTGGC TGCCAAGATG GGGGGACCCT GCCCC

C/T

GAGGCCTCAC CTTGACGTTG TGCATGCTCA TGAGGTTCCC ACAGTGGTCC AGATACTGCT
TCAGGTCAC TGCCTGGAAC ACAGAGCGTG GCT

01T399 144bp

AAGGCTGGGA GGTGCCCCCA TTCTCTGGGT TGGAGCGTGA TGGC

A/G

TCATCTATGG TCGGGGCACA CTGGACGACA AGAACTCTGT GATGGTCTGA GATGCAATGT
TCCCTCTGCC TTGGGGCCCT AAAGATCAAT CAGGATGGG

01T400 147bp

AAGCTCTGAC TTGTCTTGG CTGCAAAGAC CTGAGGTCTT CTCTTTCTAA GGCTCCTA

A/G

AAAGTGTCTT CTTGCAGCAT CTTGGCCAAT TCTCACTGGA GTTCTATTTG GAACAAGTAC
TAAAATGCAA GCCAGAGTCA ACAGAAGA

01T403 131bp

TAAATAATCC TGCAATAATT CCTGAAAAGT TGTAATCAC TGACA

G/A

TGAGCTTGGG GTGTTATCTC TCTCAGGGAC ATTTGTATTT TAATAGGAGT CTCATAATGC
TACAAAACT TTAATCAAAG CAATT

01T404 137bp

CAGCCACAAA TCTGGTCAAT GAAACACACC CAAGAACCTG TAAGATTATA

T/C

GCCAGGTTCC ATGGGAAGTG CACTTGAC T TCTCTCCCAA GCAGTGAGTA GACTGAAAGT
TTCCAAAGGT GGGGTTTGT GTTACC

01T406 125bp

AACCACCTGA TGACGTGTGT ATTAAACAAA CAAACATTTT GAAGTGCATT CTTTATAAGG
TAAGGCTTGG GAGGAAAGC

C/T

GCCCACAATT AACCTAGGAA TTAAAAAGGT AAGCAGAAAC AACTT

01T408 124bp

GCCTCAGTTT TCCCCACTGT ACCATGAGAA TAGTAGCTGT ACCTTTCTCC TAGGGTTGTT
GTGAAAGTTA AAT

A/G

AATTAAGGTG TACATGCTGG TGCCTGACGC ATAAGTGTGC TACATGTGTG

01T410 109bp

CTGGGCACTC CCAATTTCTA GTCATTCAAT ATCTATTTTT CTCCTTCTTT TCTTCA

A/G

ACCTTGTGTC TTTCATTTAG TTTCTCAATT CATACAAAAC CGCATCCAGG AC

Table III

01T411 148bp
 CAAAACCTGC AGGGCCAAAA CAAATACAAC GCATCAGAGG CCCACCTCC TAACCAAGGA
 AAGGGTAAAG GCAAGAATAA CACCAAGAGG CCACCAGCC
 T/C
 CCCATCAGAC GGGCAGGACC ATGGCGGCTC CTAGCACATA AGCCTCGG

01T412 104bp
 TAAAGCATT CCAAACAAAC ACAATTTAGG ACAATTTGTG ACA
 C/T
 ACATTTGCTT TAGCTAAGAG ATGAGGATGA TTCAAATTG AACCATAACA CGAACATATC

01T414 121bp
 GGGAGATGAA GATGACCCTA TGTACATCTT CCAGTCCAAT TATAAGGCA
 C/T
 ATATGGCCAG CCATGTGACC CACATGCCCA TAATCAACCC CAAGGAGAAG TACAAGCACC
 TAGCCATAAA G

01T415 133bp
 TCTGGGGATC TCTTAGGTGG CTGGTGATTC CTCAGAGCAT TTTCCCAC
 A/G
 CTTACCAGCT TTTCTATTAA AGAGGTTTCTG ACTGTGCTTT TCTGTGCAGA AATGTTTATG
 TCTTTTTTTT TTGAGACAGG GTCT

01t417 134bp
 GCACACATTT AATTTGTTTG CACCAAAAAA GAACAGTAGA AAACAGTCAT TAATTTAAGG TA
 A/G
 GAATATATCA TCCCTGAATA CAAAAGTAGG TATTTACGGG TCAAATGCAG AATATTCAGT
 GAACAGTTTC C

01T418 132bp
 CCTGTAGGGT CACCTGGAGC TGCAACAGGG AATTTTCTCT CCGTATACCT AACTG
 A/G
 CCAGAGCTTA AAACAATTCC AGATCTCCTG ATCTATTTGG CTGGATAACA TAAGAATGCT
 ATTTTGGTGA AGGTGA

01T420 135bp
 CTCCAGAACG GGCAAACATA TAGAGTCAAA GCAGATTGGT GATTTGCTAA
 G/A
 GGCTGCAGGA AAAGAAGATA GGGATATTGG GGATGATGGC TAAGTGGCAT GGGGTTTCTT
 TTTGAGGTAA TGAAAATGTT CTCA

01T421 123bp
 AATTCTTCAA ATCACCTTGT CGAATTGGGT GAATTAAATA GGGTTCTGTC CCTAAACTGT
 GGCTTCAGTC AG
 A/G
 TCTTATCTTC AGTCTTTTAG GTTCCCAAGG TTTGTGCAAG GGCTATCATG

01T424 124bp
 GTCAAAAGAG GTCATTTTGG AACTTTAAGG TTTAATGAGT GCCCTATTAA ATTTT
 G/A
 GATTTGCATA GGACCTGTGG CCCCTTTGTT TTGGCCAATT TCCATTTGGA ATGGGTATAT
 TTACCCAA

01T425 145bp
 GCCTTGGTAA GAAAGGGATG GGAGACAAGG CTAGAATGGT AAACAGGGTT CAGACTACAG CTAC
 C/T
 CAGTGGTGGG TCTAGAAAAA TAATGACCCA CATAGAAAAG TTAAGTAAAC ATATGATCGA

Table III

GGAGTTTTCA TAAAATAACG

01T426 149bp
 ATGCGTCTTC CCAAGGATAC GATGCACCCA CCTTCCTTCT GTCC
 A/G
 GTACCTCACC ACACCCCGTC TTACTCTGGG GCTTTTCTTT TCCTTGCAACT GAGAAGTAC
 AGTTCTCTCA ATTTTATTTC AACTTGGGGG TTGTCACCAG TGTT

01T427 131bp
 ACTTCCTGCT CATCATCAAA CAGCCCGCCA AATCCAAGTT AAAGGATCTC CATCCCAACA
 TCCCTCTAGC TAGATCCTGA ATCCCC
 C/T
 GTGGCTACCC CTGTCCCATG TAGAGGGAAG TGTAAGTAAG GGAA

01T428 109bp
 GGGTATATTC AGAGAGTCAT GGTAAATGTT TCTTGCCACT AAGAGAC
 C/T
 GAAGACTGTC GTCTGATCTA TGCAAGAGAG AGCTTAATTA GGCATAGACT GGAGTCTGTT
 T

01t429 93bp
 ACCCACATTC ATTACCCAAC TCTTCATCTG AACCCCTGTGG TGTAGACA
 T/C
 GGGCTAGAAA GGCCAGAATC CAGTCTTTTG GAATGCATGT GGCA

01T430 149bp
 TCAGTAGCAA ATATGAAGCT GTTACATACA GATACTGAAT AAAGGTTAAG TAAATCCTT
 CACTCATTCA ACAAATATTT ATT
 A/G
 CTCTAAGCTT GGTGCTAGTA TATCAGACCT AAAATTTAGA GTGCCACCTT AACATCTTTG
 AGCCG

01T431 121bp
 TGTCTATTTT TGCTTACGTT GCCTATGATT TTGGTGTCAT ACCTAGGAAA CCATTGCCAA
 AAGTAATATT TTTT
 A/G
 TATAGTTTCA CAACGGAATC CCACATGAGG AACAGAACAA TCAGTA

01T432 115bp
 GAGGGGCATG GCCAGGAGAC AATGACAGCC CAGTGTGAGA CGTGCTTTAG TGTACACACT
 TAGAAG
 G/A
 TACCAGAGAT GTGTAGAAGT AGAACTACCT AAATCTGCCT GGAGAAGG

01T433 142bp
 TCTGTGCTAG ACATGGTGAT GGGCACTGCC AATTAAATCT GTATTATAGT TTAAAGCCTA
 A/G
 GAAGAAATTC TCAAATCCAT TTCACCTATC TTAAATCTTA GCAAACCAAC CATACTGTGT
 CCGGATTGG TTCCTCCGG T

01T435 126bp
 CCCCTTTGCT TGAATTCCTA GGCTTTTGTT CTATACTGAG AATCAGCCAG TGCTCCTTAG
 GGGATATACC TTGAA
 A/G
 AATATCAACT CATCTGTCTG AGATTCCTTT GACTTCAGGA TCTTAACTCC
 01T436 148bp

Table III

AATGACAATT TCATAGCTTG GGCTTTGATG GGTAACCTGC AGCCCCACTG GCC
 G/A
 CTCCAGCAGA TGGTGACCCT GTGGGTGGTA GAGAGGCTTG AAGGATCTAG TGCATCTCAG
 CTGAAAGTGG CTTGTCTCAA ACAGATGTGA GAAG

01t437 142bp
 TCTATCTCAA GGACTGAGTT CTTTCCTGGA AGCATAGCTA GGACTTTTGT TATAGAAGCA
 AGTCAAGGAA GAGAAAAATT TTAAAGAG
 C/T
 AGATAAAGGA AATGGCCCTA GAAAAGTGAC TCCCAGGCC ACATCAAATA CTA

01T438 129bp
 CCCTCGGTTG TCAGTTGCTG GTTTTGCACA CTGCGTCAGC TTCTCCC
 A/G
 TGTGCCTCTC TGGCTGGTGA GCCTTCATTC CCCCTGACT GGCTGCCCTG TCCCTCTCTT
 ATTAAAGGAT GCCTTGGGCA C

01T440 145bp
 TCTTTTTTGG TCTCCTTTCA TCACTGTGTG ATTTACTTTA ATAGTACCCT GTCAAACCTAG
 ATGACTCAGT GGCCTCATCA
 C/T
 AGCTTACAGA GCATTTTCATC TGTGGTCATT CATCCTGCCT ATGAAGAAAT TGACATGTAG TCAC

01T441 149bp
 GGTGGGGTCT TCCTATCTTA GACCCCTGTA TTATATAAAG GTACACAGTG CACCTCTTCA
 TAACATTCAG TAGT
 A/G
 TGAATAATGA CTCACTGAGT CCCTGTTTTT CCCATAGAGT TCCAGGCTCC ATGGAGTTCC
 AGGCTTCATG AGGG

01T443 140bp
 ACTCAGGGTC CAGCTCTTAT GCTCCTGGAA CAGATTGTTC CAAGGTTGAA TTCAGACCGC
 C/T
 GCCATTTCTT TGCTCCAGGC TAATCTTAAA TGTTCACCT GGGACACTGC TTGCTCCAGC
 ACCACTCTTT GCTTATACT

01T444 133bp
 GTCAAGTTAT GCGGAAATC CTATTAGAAG TATTTCTTGG TATT
 A/G
 GACTAGATTT GTAAGTTGAT TGGGTGCAGT TGAAATCTTT AAAAACCCT ATTAAATTTG
 TGGATTTAAG CCCAAAAGAC CCTAAATA

01t445 145bp
 TCCTACTGAA GTGGCACCGG ATTTTGCTGT TGGGGGAATG CAAAAGGGTC AGGCTTCTTC
 ACTCTCTCCA TGAATCAGGG GTGGTAGGAA CAGAGGCAG
 C/T
 GACTGCTGGG AATTGAACTC ACAGAAGAAA GCTGAATCAT GGCTC

01T446 144bp
 GACATTTTAA AGGCAGCAA TTCAAACTA TAACTCAGGA TAGACACTGA AACCATACTT
 C/T
 GCACCAGATT AAGAAACTG GCTGTTGGTA GTTATCAGTG AGATGGCTTC TTTTAGAAAA
 TTGTTGGCAA TGAAATAAT ACT

01T448 125bp
 ACTTGAAAAA TGTATTTCAA ACCTGCATAT TTCTCTGCAT CTCCACAGCC ACCACGCTAT
 TTAAGCC
 G/A

Table III

CTGTTATCAT CACCTGGACC ACTGTGGTTT TCTCTGTTCC CTAACGCACC TCTTTTC

01T450

CTTACCAGCA CTTGATATTC TGCGCTCTCT CTCCCATTCC AGCTGTTC

C/T

CTTTCTAACT GCTCTTGTCT CTCCCTTTC TTGCCTCTCCC GTTCCAGTCT CTCCAGCCTC

01T454

144bp

CTAGACTCAA CTGGCTGGGT CACCGATGGC CATTTCATCT GTGCGTAGCT ATAGGGATTT

AAATAGGAGG ATTTTGTGA AATGAAGACA ATTGACC

A/G

ACTGTGCGTG GAATCAATGT GCAGGATGAT TCACCAGGCT TTCTGC

01T455

147bp

CTCCTGACCT GAGGTGATCC GCTCACCTTG GCCTCCCAA GTGCTGGGAT TACAGGTGTG

AGCCACACCG CACC

C/T

GGCCAATAAT ACATTTTAGT TCAAGATTAG TGAGAGCTAA GGAGAAATGA GAATGCTGAT

TGTTCTGAAA TT

01T459

120bp

ACAAACAGAA GCTACATGAC AAGTTTTGCT CTGTTCAATT TTTCTCTTTA AACTCTACTG TGT

A/G

CTGTTTGGA AACGCTATTA TTTCAGAAGG GAGAATCTCA TCTGGAATCA GAAGAT

01T462

149bp

CTGCAAAGTA GATATTCTGA ACCCTCATTT TACATTTGTA GAAACTGTAG TACAATTAAG

TGATTTACCT TGGACCAC

C/T

TCACTATCAT TTGAATCCAA TTATATCTAG TTGCAAAGCC CACACTCTTT CCACTACATC

CTGGTAACTG

01T464

145bp

AGGTTAGAAA AGCAAACAAA GGTACAGTAT ATCTACAACA CCTTAAAATT GCCACTGAAG

TTTAGATTTA CAAGTCAC

G/A

GAGTTTCACT TAATTTCTGC CTGAATATGT GTGAACACTC TTGGGCCATG AATGCCGAAC

AAGGCT

01T465

137bp

TATTTGCAGT GTTTTCTGAC AAATATTTTT CCTCCAGATT TTAAGC

A/G

TGTTATGATG AGTCAACCTT TATGTTTGTA AAGCCTTAGT CTTGTTAATA ATGTATAACT

TCCAAATGAA TCATATACTT ATGCATAGCA

01T469

125bp

GCAGCAATTT TAGAACC GTT CTAATTTGAG CCAAGACATT GTCTTCATAT GCCCA

C/T

ATCTGCTAAT CAATGGATTC TGCATGCCGC TGGATGGAGC TATAACCTCC AGCAGGGCAG

CTGCCTTTT

01T470

115bp

ATTTGAAATT CACAAGTGTG GGTATCAAAT ACACATAGGT GCTCTTAACT CAAGGATAAT T

A/G

AAGCATGAGC TCAGGCTCAG AGAGGCTAAG AGATTTGTCC AAGATCACAT AGC

01T471

133bp

Table III

TTCTTCCTCT CTTTAGCGCC TCCCTCTCCC TCTGCTATTG CTTGCCATGT TGGAACTGTC
AATCACGGGA TCCTCTCCCA CTTTCA

A/G

CAAGGGAGGG CAACTGACCC AAGCAAGGCC TCTCAGACTC CTCCTC

01T473 131bp

TTTTGAACCA CAGGCCTCAT AACTGAAAGT AGACTCACCT TTTTCAATAA TAGATGACAA
AATGTCGGAA TGTTTGCTTC C

A/G

AATATTTTTTA TTTGGCATTTC ATCCTGAATC ACTTAATATC CCTGTGATG

01T474 143bp

CTGCCACACC TCTGTAGCCC AGAAAGGAAA TTTTCATATT TACTTCTTTA GAGAAACCAA
CTCCAGTCAT CTACAG

C/T

GCTTTCTTTT TTTCTGACCC TTGGAAAAA TGTTATTTGC CACGTTTTAG CTCATACTGC
TGGCCT

01T475 14 bp

CTAGAGAGGG CCTGACAACG AAGCTGTTGT GTCAGGGAAA TGAACAAGCA GAATTGTTTT
TTCATTGGGC

A/G

GGTAATGCAT TTATGTTTCT GAGGGAATGG ATACATCTTT CCGTTTATTT TTTAAGCAAG
TAAAACAAAC AAAACAA

01T477 107bp

CAGCCAGACC TGCCCTGACT ACAACCCCCA CACTTCTTTC CTGTGTGAGA AAG

C/T

AAGCCCTGGT TCTTTCCGTT TCTATAGCAA TGTTTTCTGT TACGCGTAGC CAA

01T478 143bp

GCTGGATGGG ACCAGAAAGT GAATACGCCG AGGCATAGGG TTGTAGCAGA GAAAGAGGTT
TCATCGTAGG G

C/T

CACCGAAGGA GGAAATGGGA GGAAACGTCA AATCCATCTC CCTGAGGAGT TTGGGGCTGG
GGTTTTTAAG G

01T479 106bp

AGAAGGGCGA GGAAGGACTC TTCCCTGGGG CCTTCAGAGG AAGCACAGCA C

G/A

GCCGACACCT TGATTTCAGA CTTGCAGTCT CCAGAACTAT GAGAATACAT TTTT

01T481 134bp

CCTGGGTCCA TGTGGATGGG CCTTGAGTTT GAGTCCATGG GGTTTAGCCT GGTGCT

A/G

GGGTGAGCCT GGAGCTTGAG TATGCAGAAA GAGACCTGGT TCTTGGGCCT GTGGGGACCT
GTCTGGATCT TGGGTCC

01T482 147bp

GTTTCCAGCA AACTGTGAC TGTACTTTTA CCAGAAGAAA TATATTAGTG TAACAGATGT
TGACTCTACT GTAGAAGCTG TGTG

C/T

TAAACCTAAC ACATGCCTAC CAAGTAAAG TAACTAGTTT TGCTGTTTTG TTTTCTCAGT
GC

01T485 148bp

AGTCATGACC TAAATTAAAC AGCATATTCA ACTTAACAAA TTCCTCTATA AACTT

Table III

C/T

TATGGATCCA CTGAAAAATG GCCATCTGTT TCCTTTTATG AAGTCAAATC ACATCTAGAA
 AATGGCACAC ATACCGTAAG TGTTCCCTCA TT

17D143 not use Bsl1

CTTCCTAACT CGGGGGGAGA ACGGGGCCAG GCCGCCCAGG GGCA

G/A

GAGCTTTAGA ATCAGGGTGA CCCCCACCCC TACTCCCCAA GCACAGTCAC

17D256 116bp

CTCCCAAATG GATATTCATT CACTGCATTC ATCTTACCTT TTCTGAATGC A

T/C

CACATTTAAA GCCGCACTAT GGGGAGCCAC GGATACATAG TCACTGTCAT TAATCATCGT CACC

17D279 108bp

TAGAGATGGA GTTTCACCGT GTTGCCCAGG CTGGTCTTGA ACTCCTGGGC TGAGGTGAT

C/T

TGCCAGCCTC GGCCTCCGCC TCCTTTTTGT CTTTACATCT TTTATCGC

17D350 142bp

GATCTAGCCT CTCTCCAAAC CCTTCTTTTG TTATAGAGTA TAAAATTCTA GAGTGAAAAC TAA

A/G

TTTCATGGCT CTGAAGACAT TTCCCTATTG TGTTTTTATT ATACTGTACT TGAAACTATT
 GCCATTGTGT GATACATC

17D402 139bp

ACTCCAGCCC GGGTGACAAA GTGAGACCCT GTCTTAAAAA CAAAAAAGAA AAAAAAAGA
 AACTTGTTGG CTCGATTTC A GTGTTCTTCA

A/G

ACTTTGGTTG GTTGAAGTGA TGTACTATTG CGAGGGAAAA ACATTCCA

16_001 125

CCTCAGTGCA GCTCCTGGCT TACCCTCTTA CTGTGGGGGA TTTACAGGCT
 GGAG

A/G

TTGGGCCGGC ACCTTTCCAG AGCAGTCATC CCTCTGACAT GTTCAGGGAA
 TTGCCCAGG TCTGCCATGG

16_002 139

TGCTTTTTGT TTTCCCAAG TGTGCAGCTG GTGCTGAGAG GTGATGGTGC
 TGCTTGTCCT CACACAGGAG GAGGAAGGTG AGGACGGCGA TCCATC

A/G

TCAGGGCCCC CAGGGCCGTG TCACAAGCTG CCTCCCGCCC CC

16_003 106

AGGGTTGGGC AGTGAGACGC GGCTGGACCG CAGCAAAGGA GATGC

A/G

CGGAGCGACA CAGTTCTGCT CGACTCCTCG GCCACACTCA TCACCAATGA
 GGGTAGGCTG

16_004 127

GGGCCACTTA GGCGGGCAGA ACGCAGGGGC CAAGGAGCAC CACAGGAAGA
 TCCCAGCCCC GCTGGCGATG G

G/A

CACCTGCGTG CAGGCAGAGG GCAGCACATG GAACAGCAAC ACAGGCCTGC A
 ACAGG

16_005 145

Table III

GTGCGTGTG ATGAGTGGGT CGCACCAGGG TGGAGCCTCC TAGAAGGGCA GGA
C/T
GCACCATCCT TGGGGAGTGG CCTGGAGAGG CCTCGGGAAG GGGGTCCAGG
GTGGCTGAGC CTCAGCCATC ACCCATGCC GTCCAGCCCT

16_006 108
GCACAGCCCA GCAGGGGGTC CTGGGCCTCG TCTGCCAAGC CTGCTGCATG CCTGG
A/G
AGAGGGGTCA GCTCTTGGGA CTCTGGAATC TTGAGAAGGC TGATCCCTGG TG

16_008 147
GGATGGCTGC AAAGTGCAGA CCGTCTGTGC ACGAGGGATG TGAAGAACA
TCTCCCCAA GTTCAGAGCC AGTTCCAG
G/A
GTGCAGGCAC ACCCACGCAG AGCCCTGCCT CCCCTAAGGA GGGGGGAG
GTCAGCAGGG TCCAGGC

16_010 115
TGCGTTAACT TTTTCGCAGA CGGGAAACTG GGCAACAGGG AGGCTACAGG
CCTTGCAGGA GGCCATCGGC
A/G
AGTCCGATGC TCAGAGCACA AACGCCTGGCC TAAGAGGTGG TGTC

16_011 118
AGGGTGGAA TCTCTGTTAA GTCCACCCTG CCCAGGGTG CTCCTACCCT
CTTGGTCTTT TTAAAG
C/T
CAAGGTGCGA TTTGGGCACC TGA CTGTCCA GTTTACCTTA ACAAGTTTGG
GA

16_012 145
GTCTGAGTCT CGAGTATGTG ATTGGCCAGC ATCTTGGGGA CGGTGGTG
A/G
AGGAGAAGCA GATGTCCACA AAAGACAGGT TGCTGAGGAA GAAGTACATG
GGGGTGTGCA GGCAGGAGTC TATGCTTACG GACAGGATGA TGAGCA

16_013 96
CCCTTCTCCT CCCAGCCGGA CCAGACTCTG CGCACCAGG TGTGGGCT
C/T
CCTCTGTGCC GGGGTGTCTC CACTCGACTC TGTTGATGTT TGGGATG

16_014 135
ACATTCTGTG GACTTGGACA AATGTATAAT GATGTGCATC ATT
A/G
TAGTGTGATG CAGAGTATTT TCACTGCCCT AAAAGCCGTC TGTGTTTCAC
CTCTTCATCC CTCTCTCCTT CCCAAAACCC TGGCAACCAC T

16_016 149
CATCACCTC CAGAGCTGGA GGGGACGGCC ACCCATACCA AGGTCCTTTA
GCTGACACCT AAAC TCAGGA GCTAACCATG TG
C/T
AGGTCACACA GGCCGAATCA CAGCAGTGAT GAGACGCTGG GGTCTCCACA
CAGGAACCCA ACTGAC

16_017 123
AAACCAAGA CAGCTGAAGC GGGCTGTGCG TTTGTCCCC AGCTAGGCCC
AGGGAGTGGG CATCTGG

Table III

A/G

ACGCAGGATC TCCTGTCCTC CCGACACCTC ATTACCCATA TATGGGCACC
AGCCT.

16_018 115
TAATCCAAAC AAAC TAGAGG CTAATTGCCA TTCCCAGCA CAAAGCTGCA
GTGACGATGA TTCTTTAATT C
C/T
TTCTACGTGC TCACAGCCCCA CGGCGCTCTA CTCTGCTCAC TAA

16_020 117
TACCTGCACC AGCCCATTTCT AGACCTGGCT CTCTTTCCAG GCCAGG
C/T
GGGAGCTCCC GAGAGGGGTC TAGGCATCCC TGAAGTCCAG GCCTGTACTA
TTAAGCAGCT CATCCTGGTT

16_021 132
TCAGAGAAGC CTTATGCCGC TCGATTTCCC ACCAGCTCTG GAGTCGGGTC
CTCTCCACTT CCACACATTC
A/G
TTTCCACAAG ACAGGTCACC TTTCCACCAG TGTGGACGTC TCACAGTAGA
ATCAAGGACA A

16_022 98
GGAATGCATG TTTCCCCAAA CATGTACTCT CGGAGGTCAT ATTAGTCT
C/T
TTGCTTCCCT GCTCTTTTGT GACAAGCAAT GTTAGGATAG CAGTGGATG

16_023 128
TCTCTCCTTC TGACTTCTGC GATGGGCCGG GGAATTTGGT TTACATAAGC
AGCCCCGTTT CTCAGACCCT
C/T
TGTATCTTCT TCTGGAGTAT ATGAAGGCTG TGGTACCAGG CCAAATTTTG
CACACAA

16_024 121
AGCCGGGTCC CTTCTCATC AGTCACCATT TAATGGAGAC TGAATGGTTG TGGATAC
C/T
TTTGTTAGGG TCATCAAGAA GGTTTGCCAT GCTTGGCTTG GTAAGGAGGA
GGTTGTGTGC TCC

16_025 89
ATCTTGTCTT CCTGTCACAC CCACCTGGCA CCACCTTCCA CCCAGCT
C/T
TGAGTCAATC CACCACTTCC TCACCTGTCA ACCACCAAGC CTCATTAC

16_026 105
TCTCCACATT AGGGCAAAGT GAGCTCACAT CTCTCTTACC TGCTCTCTGG
GCCTCCC
A/G
GCCTGGACTC GCACAAGGGC ACCATCCCAC TACCCCTCAT ACTTCCA

16_028 92
TGCCCCACGG GCCTTACCTA GTCCCCGAGA ACTTCCGGGA GAG
A/G
AACCTTCAGC TCATCCAGTC CATCAGGGAC TTCCTGCAGA GCGACGAG

Table III

16_031 136
TCCCCTCCTA ATGTGTCAAT GGCTTTGCCA GGAATTGCAT CGGTGGTGTG TCAGG
C/T
GGGCTGTTGT CTGGTTTCTG TGACAGAGAC CCTGAGCAAC ACTGGTTTAG
ACAAGGTAGA ATTTTCTTTC TTCCCACTTG

16_032 149
TGAGGCAGTT CTGTGAAATC CTCTGCATGG GCTTTTGAAA TTCCAAGGTT
CTCTTCTTAA GGGCAGG
C/T
TGCACAGTAA TTTCCCGAGG AAGGCTTTGT TCCATAAACC CAGGCCTTAC
AAACAACAGT TTCCGCCTCT GATATGTATA A

16_033 141
GCATTACTCT AGAATTGGCA TCAACCCCAA GCAAGGGAGC AGGGCTTTCA
TTCTTATGTG CCTA
C/T
GAGTCGAGTC ATTCACCAA GAGATGGAAA CTTCTAGCTA CTCTGGCTCA
TTGCATGTTG AGGGAAAATT TCTCCA

16_035 120
CACGCTCAAC AGCTGTTCCC CTAGCTGTAT CAAGTCCAGG CCAGTGAGCT
TGCTTCTCTC C
A/G
GCTTGTCTCA GCAATTTTGT TTTCCCCAC TGCACAAGTT CCTAACAGCT
CCAACGAG

16_037 147
ATGGGCGCAT GGGCTCTTTT ACAAATGTGC CGTGGTCCGT GCATTGTGCT
GCTGTTGTGC CCTCTGCTG CAA
C/T
GGCAAGGAAG TCCCTTTGCC TTGCGTACAT GGAACTTGGG TGCCAGGCTC
CCAAAGCAGT TCTTCTTGTG CCC

16_038 127
ACTCCCCCAA ATCTGGGTTC GAATCCCAGC TCCACCACTG CAAGTCTGGT
TGCTCTGGA
T/C
CAGTTACTTA ACGTTCTCTA AATGTCAGTT ACATCCGTGA GATAAGCTAC
CTCGCGGGAC TTCATTC

16_039 111
TTGCCCTCT GGAGTTTACA GTTCGGGGGC AGAGACAATG AATAATGAG
A/G
CAGATAAGTA AATAACGGTT TCAGATAATA-CTAAGGGCAA TGAAGAAAAT
AGTACAGGTG A

16_040 143
CATCTACAGG GTTCCTTCGG GCTATGTTTC TAGGGTGAAT GGCTGAGATA
TAAGTGATGT GCTAT
C/T
CAAGGCCTTT GATCGGTAGT GGGGGAGACT CGGGGCAGGA GATGTTTTTG
GCGTACCCTG AGACACCATC ACATCAT

16_041
GGGTTGCCGT TCTAATTAAT CTCTTATCAG TGCAGTCAGG GGTCTCCTTT

Table III

GGAGCCTCTT GTGGGGGTCC CACTTCAGTA GTTACTAGAG CAGCTTT
 C/T
 TGTTACAGAG GTCCCCTTTT GAGTAGGTTT ATAAGGAATG TGAGAATT

 16_043 124
 CACACTGAGG CAGCACCTCC GGGGAAGTCT CCGTGCTCCG ATGCTGTGGC C
 A/G
 TGTACAGCAT ATGCAGTCCC CAAAGGGATA TTTCAGCACA GAGTTTCAAT
 GTAAAATGAC ACACGCTACT GC

 16_044 135
 GCATAATCCT TAGCACTTGA AGACTTTTTTC AGCACCAAGG ACAGCAAAAC
 GTCATCGTAA TCAGCACCCA
 C/T
 AAGCATCCAC CTTAGGATTG CCTAGGGGCC GGCCGCTCTC ATAAATACAT
 AAAGGGGAGG AAGG

 16_045 138
 AGGGCGGCCT CTCCTGCAGC ACGAGGCCTA CCTGAGGGGC AGTAGGAGGA
 TGAGTTGGGC ATTCTCC
 A/G
 CGAGAAGCTC TTGACCACCA GGCTCTGGCC CCACTGCTTG CGCCGCCACG
 CCGTGCGGCA CTTGGAGTCG

 16_046 137
 TCCAGCTAC TTGGGAGGCT AAGACAGGAG AATCGCTTGA ACCTGGGAGA C
 A/G
 GAGTTTGAGC TGAGCCGAGA GTGCGCCATT GCACTCCAGC CTGGGCAACA
 AGAGTGAAC TCCATCTCGA AATTAAAAA AGAGT

 16_047 106
 GGTGAGGAGC CTGGAGCCCC ACGCTGGGCC CGAAGGTTCA AGGGCTTCTC ATCAG
 C/T
 GGCTTCTCAT CCGTCTCACC CTGGTCTGCG GCTTCTTCTC TAAATGCATT

 16_048 111
 AGCTACTGGA TGCACTGGGT CCGCCAATCT CCAGGGAAGG GGCTGGTGTG
 A/G
 GTCTCACGTA TTAATAGTGA TGGGAGTAGC ACAAGCTACG CAGACTCCAT
 GAAGGGCCAA

 16_050 133
 ATCAATTTGC TGCTGTTTAG TAAGGTATAA ACTACAGTTA AGGTAAAGA
 CCTTGCCACA TTCTTCCAT TTA
 C/T
 AGGGTTTCTC TTCGGTAGGA ATGATCTGAT GTTGAGTAAG GTGCAAATA
 TGGTTTAAG

 16_051 145
 TGATCTCTCC AAGGACTGGC CTGGAAGGGA CAGAGAAATG CGAATGCCCT
 TT
 A/G
 AAATACTCA CAGCGTATAG TTGAGTGGTT TCCAAAGACC CCCTCTATGC
 TGCCAAGCCC TAAGCATGCT CTCGTATCTG TTGTTGGGAG AT

 16_052 98
 AAATACTGAG .GGGTTGGCAT GAAAGACCCC CACACCCTGC TGCCTGCTGC

Table III

A/G

GGAATTGACC AGGGCATAGG CTTAGAGGGG CCTCATCAAT AATAACC

16_053 125

CTCTCCCCAC TAGGACAGGC ACGTGTCTC ACTAGGACAG GCACGTGTC

T/C

TCATTGTGTG TAGGTCAACA TGGAACCTTC TCCTACTGCT TGCTTTGGTA

AGAATGATGG GTTATCGGGA GGCTG

16_054 116

CATCTTGATG CACCAGGGTG GTCCTAATGT TCTCAGATAC ATTAGAATCA CACAAT

A/G

TGGTCCCTAA ATGAGAGCCA ATTCTGTCTT GTCATCAACC AGAGAAACAG

CAACTTGT

16_055 113

CCTTGCAGTT CCCAGAGATG GTTAGGGAAG AGGGACTCCC AGTCAGCAAC A

A/G

TGCGATCTTG TAGTAAATGC CAGTCTCAGC TCCAGGTTTG GTTTGACCCC

ACATGTGTTG G

16_056 131

TGAGGGTTCT GTGCTTTTCT TGCTCCAATG CTGAAGAATG GCCTGCTGCT

TTCCCAGGTG TCACGGGCAC TGAGAAAGGG CCCC

G/A

TGGCACCAGG AGCTAATCCT CAGGGGTCAG AGGCTGTGGG AGATTC

16_057 139

CTGGGCTCCA TCCTCCCTCT GGCCTCACCT CCCCAGCCAG CCCAGG

C/T

TGCGCCAGCA TCTTCTTCCT CGTCCACACC CTGCCCTGCC ACTTCGCTCT

CCTTCTCTCT TGGTCCCTGC CCCGTTTCTA GCATGCCCC TT

16_058 143

CTTAGCCTCA GAGGTGTGCA TCTACTCACA GAAGGGCTCA GTGGCTTCCA

GTGTTCAAGG TTACTGGATT GCACA

G/A

GAGCTGTTAT AGGACAAGCC CCGTGGATAC TGGTGGCTCA GAGGTCTTAC

AGATGAGGTT TCACTGG

16_059 138

GCTTTCTGTG TGA TAGTCT TCTAACTGCT GTATAGACCT CCAGGCTTTG CCT

C/T

TCCATCCTGC CAGTGACACC AGGACTGCTG CCACCATTCA TGCTGTGCGG

ATCATTATCA TCCATGTCAC CTTTAGGGCC CACT

16_060 117

CGGCCAAACT TAAATTTTAA AAAGAGGAAC AGAAGTCAGC CAGACCAACA

AAAGAGCGAC

C/T

GGTGTTCCAA GCATAGGAAA CAGAGGAAAC AGAGGCCAAA ACCTCGGGAC

TGTGGA

16_061 125

GAGCCAATGG CCAAGAAACA GTTAATAAAA TAACAGACGA TGGTCCTGGC

CTCTACTGTG AGTGAGTAAA G

A/G

Table III

- 38 -

GCTTGCCCTG CAGAGATTCA GTGATCTGGC GGGGGTTGCT GAGCTATGAG
GAA

16_062 100
ACTTCTTTT CTTGTCCCTC TCATCTAGGC ATGGCCATGC CTCTTCAT
C/T
GACTCCTGTG TGTCCCCTCC CCATTCTTGC TGTCAGACAG CGTGCTGGTT
C

16_063 140
ACTTACAAGT CTGGGGTCCG GGGCTCCCCG GAGCTGGAAG ACCAAGGCCC
CTGTGCCTGG GATCGCTGGG TTA
G/A
GGGCGGGTTA ACCTAGGGGT CCCAGCCTCC AAGTCTGGGG AGGATCCGGG
TTCACGGGGT CGGAGT

16_064 119
ATAAGTGAAT TCCGCTACGA TGGCCAACCT CTGCCAAACC CAACCTGACC
AGTGGCCAAC CTGAGCATCA CG
G/A
TGTTTCAGCCC ACTGATGGCT GCCTCCAGAT GCTCCCTGAA GGGACA

16_065 141
TTCTCTGCTA AAATATTGCC GTCTCAGTGA ATCAGCTCTA GATGAACTCA
TTGGGTGATT GTAGGAGAAG CCCCTCCCTT TGGGGCTTGG AGAACC
C/T
TGGAAGGAG AAAGGACAGG TGGTGGGGAG AGGTGGGTTT CCCT

16_066 112
GTGACTGTTC CAGAAGCTGC CTACTCTTCT AGTGCCTGCA GCAATC
C/T
GAGGTGTGGA GGGCACTCCC ATTTCCCTTC CCTGTGCTTG AGAATCTGTA
GAAATTGTGC AACTT

16_067 119
CCACTCTTTC CTCTGGCTTC AAGTCACAGT GTGCCAGCAT CCACATGGGT
AACTCAGGGA TGATG
A/G
AGCTGGTCCC TGACAGGGCC TCACACCTCT CGCTGGTGGG CACTGACCTA
TCC

16_068 123
ACCAGCTTTT CCCCAGGGG TTAGCCCAGG GCCTTTCGG CACCCAGAT
C/T
GCATCTTCTT AGCTGTGCCC CAGAGAATGA GGTCGAGATT GTGATCTGAA
ATATTTTCAA GGCAGGTGCT GCT

16_069 113
CCAAATAGCAC TGTGCTTGAA TATTAGATCA AGAAATGGCC TGACAGCCCA
AGACCCCTTC TCA
A/G
TGAAATTAGC TTGAGACTTC TGACAAGAAC GAAAGTATTC TGCCCAATG

16_070 106
CCTCCAAGCC TCTGCACCTT CTGTTTCTTG TGCTCAGGCT TCCCTCCACC
TCCACCC
C/T

Table III

TTTGTCTCA TGGTTGATGC TTCTTCTCCT ATGCCATGTA TTCCATG

16_071 115
ACACTCATAT CCACCTTTAT CCTAAGTCCC CAGACCTAAC TAATGCCTTC
TCAGT
G/A
TCACCCAAAG CCTAGGTCTT CCCTTATTCC ATGGGATAAC TGCACACAAA
ACCAGGATC

16_072 122
ACATGTTTCC TCTCCCACTT AGTTGGGGCC AGGCCCTGGG GAAGAGAGTT
TGCAAGAGGC CCAGGTTTAG
C/T
TGAACACGTG GAACCATTGG TGAGCTCCTA GCTCCTGCAG TCCTCTTTCC
A

16_073 138
ACTGCAGCTG CAGAATGACA GAGGCCATGT CCAAATCCC TTAGAGACAC TG
C/T
TGTCTTAGAG TTGTTAAAT AAGAGCCCC ATATCAGGTT TAGAAAATAC
TGTCACCGAA CGAACGTCGC TGTCTCAGC TCCAC
16_075 100
TTTAAAGCCA CTGAGTTTGT GGTAATCTGA GGACCCTGGT GTATG
A/G
CAGATGCAAT TGACAGCAAT AACAACTTAA GCATACCCTG TATGGCAGAC
ACAC

16_076 143
TGACTCGGGC TGGGTGTGGA TTCTCACCCC AGGCCTCTGC CTGCTTTCTC
AGACCCTCAT CTGTCACCC
C/T
CACGCTGAAC CCAGCTGCCA CCCCAGAAG CCCATCAGAC TGCCCCCAGC
ACACGGAATG GATTTCTGAG AAA

16_077 146
CTTGGGGGAA GGTGTCATGA TTGAACACAG AACTTAGATC TGAGCTTCCT
GGCAGC
C/T
GATGGAAAAA GGCAAATCA GTGAGCGCAT GGCTCACATT CACTCCTAAA
AGGCAGCACA GATGAGATCG TAAGGCAAAT GGCTCTGCA

16_079 145
TATGAAGATG AAATCAGCGA TTCAAAGCA CAGCTAGCTG CCATCACCTT
GATCATTGGC ACTTTTGAAA GGATGAAGTG CTTAGTGAA GAGAATCA
C/T
GAACCTCTGA GGAATCAGTG TGCCCTTGCT GCATCCAAAC TTCTAA

16_080 145
ATCAAAAGCC CATAGCAAAT TCTGTTCTGT TCTTGGGGAA GCTGACAGTC
TGATTTGGAG GCAGAGGACC CCAAATACAG GCAGCCTTCA CC
A/G
ACCCTGACTC AGGCAGTGAT ACTGCTGATG AATCTGTGGT TCCTGCCGGG
AG

16_081 121
AGCGTCTAGC ACCTGGTACA AACCGATGGC ATCTCCCAGG CATTTCTGAA
CCATTTTCAC.

Table III

A/G
TGCCTCTACT CTCCGGCCGT CTCCACACCA CCCTGTGTTC TGCCAAAGGG
AGCTAAAATG

16_082 144
AAATTCAGGG TTTTCACAAA CGTAGTGAAT TTTCAGCTTG TAATTTGCTG
TCTCCGGTGA GCG
C/T
GGTGCTGAGA AGACCCGTGA TGCTCTCTTT GAAGCCCATT TGCGGCATGC
CCCAGGCCTG GGACCTCCAT TAAGCACCAG

16_085 131
AGGAATTCAG AGCTGAAAAT GACAGGAGAG CTCCTCTGGC CATTTTACGG
ATGAA
A/G
CTAGAAAGAG CAAGATATTG TCCAATCTTA CAGGGGAAAT GAGCAGAGCC
AGGAATCTCA GGCTTGAGC TGGGC

16_086 149
TTGAGCCTGG GGGGTCCCCT CGCCAGCACA AGCGCCGGTT GGCAGCAGGG
CTGGGGCTTT CCCTGAGGAA GGGGAGGAGG TAGCCCTGCA TGTGAC
A/G
GCGTGGGACA GTCCAGGCTG CACCTCCTCT CTCCAAGAGT GTGTCTGCAG
GT

16_087 145
GCAAGGGAAA AGATGTATCA ATTTTCTCTA TAAATGAAGA GGCTGTTGCA
TGGATCTGAG AAAGCCATGG GGTGAAAGGG GACAGGCCTC C
C/T
TAATGTTGAG TGACAGAGAG AACTGCAGTG GTAATCGTTA ACCAAACCAC
CTG

16_088 149
AGTCCGAGGG ATGTAGGTGA CAGGGAGGCT GCTCAGCTCA GCCCTGCCTG
CCTGC
A/G
CCACCCAGGC TCCCCAGGG AGGTCCAATC TCCCACCCAA GGCAGGACAA
GGCAGACGAG AGCCTCACGA CACCGACAGT GACGCACACT TCC

16_089 139
CATGACACTG AGTGAGGGGC CCCTTAAGGG CTATGGGTAC AGGTAGG
A/G
ATGCTAGTTG TGGCGAAGAA AGCTAGAGCT GATTAATTAT GCAGGCAGCC
CCACCTCTGC AAACCACCCA TCTGGGAGGT CAGCCTGCAA A

16_090 124
GGATGGGGGA GGTGGCCCTT AATTCTGCCT TGAGAAACCC CGCCTGAGGC
CTCAGCACCT CTTGTCCAG CCACCCACA
A/G
GTGAGGGTCA ACTCAAGTGC CTGAGTGTCC TCTCTGCACC CTGA

16_091 136
TTTGGGGCAG CCAACCTGGC ACAGCTAATC AAAGACTGAC ATGGAAGCCA
CTCCCTCTCC CCTCCCCTGT ATCACTGACA CCATTTTCC
A/G
TCGTCTTGTC ATCGCAGACT TTACAGTTGT TGTGATGAGT CTAATC

Table III

16_092 108
 GTTCATGTGT CAATTACCTG GTTACTTAGT AACCAAGTAA TCCAGTAACC
 AAGAAGTCAA GCC
 A/G
 TAGATTAAAT AGTCCCCAAC CGGGCAATAA AAAGGTCCCT GAGTACAAAT
 TTGC

16_093 85
 CTACAACCCT CAAATTCAAG TGACAGAGCT GGGATTTTGC AC
 A/G
 TGCACATCCA TCAGTTATTG AATAAGGCTG CTCTGAAAAG GG

16_094 149
 ATCCAAGAAA TTAGACACAG CCCTAAGAGA AACATGCAGA AATGAGCAGA
 ATAGACCCCA AATAGATCAA AATTCTGTCC CACCCTCTGC C
 A/G
 TCCCTCTCAG AATGGAAAGT CAACAGCAAA ATTAAGTTTG GTGGTGAAAA
 AATAACT

16_095 119
 AAGGGAAAGG AAGAACATAT GGGGAAGGCC AGAGTGGAGA CAGGCAAACC
 AGAGCCTGAA AACGAAGC
 A/G
 TCCTCTAGGT TAAGTTGAGA GTGTAACTT TAATCAGAAG GCAACAGAAC

16_096 137
 TGCTTCCAG CCTGGGCTCA GGTGACTCAA GGGAGAAAGC ACCT
 C/T
 CCTCTCCCCG CCAGGGAGGT CTCGCCATGT TTTGGAATCA GTACCATTCC
 CTTGGGGCTG GGGGGCAGCC CCCATCTCTG GACCTGGCTG GA

16_097 126
 AAGTTGTAGA TGGCCAGCTG GTACCATGGA GTCTAATGAT GCCTCATCTG
 TCCAGTGCTG ATCTTCGACA TTCCC
 A/G
 TGTCTGGGAT GGGAAATCCA TTTTGTAGAA CGAAAGGAGA CAGAAGGCAA

16_098 130
 AGATGTGTGG TCATTATCAC ACCGTTTGGT TTAATATTTA GCCAATGTCT
 TGGTCAGGA GCCTCGTACA ATGGCTCTCC ACAATCCA
 A/G
 CACTACGATG ACATGTCTTT CTAACCTTCC AAACCACACT G

16_099 137
 GGAGAAAGAA AAAAAAACC TCAATTTCCC AGTGAGCTCA CTGCTTGCCT
 CTCTTTCGAA GTTCCAAATT GCCT
 C/T
 CACTTTCTCA GAATTCCAAT CAGGGCTCCT TCAGAGGAAG CAATTTCTGC
 CAGCACATGG TC

16_100 148
 ATTTAGGATT CCTTTGTTCT TGGAAAAGAC AGTGGCCTGA TTTTAGGAGC
 A/G
 GCATTTCTG CTGCCCAGCC TGCCATTTCT ATCACAATGG TAGTCAGTGA
 GGGTGAATGT AACATTGCCG TGACTGTGAA CAGGAGGTAG CCCCATG

16_101 133

Table III

CACAGGTTTT GCCTGTTTTG CTCTCAGATG TGCTCTAGCT CATAAGACAG C
A/G
TCAGGCATAC AGTAGATGCT CAGTAAATAG TTGCCAGTTG TGTGAATGTA
GAACCATAACA TCACCACAAT GCTGTACTAA T

16_102 133
GCTGTGTCTG CCGAGCCCAG CGTCCTCACA CAGCCCTGCT GCCACCCAGC CA
C/T
GCTGGCCCAC ACGTCCCTTA GACAGCCGGC CACCTCCCGT CCCACCCCTG
CTGCTTGTTT TGTGCCCTCA CAGGTTTGCA

16_103 144
CACTCCTGGA TTTATGTGAC TCCCTTAGCT AACTTTCCC AGCCCCCTGG
GATGTTCCCC ACTCATCCTA TTCAC
T/C
CACAAAGAAA TATTGTCAAA ATCAATTGGG TGATGATTAG GAGCCATTAT
CTGCCTGCTG TGCTGAAA

16_104 139
CACCTTGCTC TCATCTTTTT ACTCCTTTAA TGCTGACCTC TGCCAAATTG
AATGAT
A/G
TATTTTCACA TCCTGACAAA AGGAACTGAC CATAGCTGAT AGAGCCCCAC
ACCTCCTTAA AGAAAATGTT TTGTGAAAGC TA

16_105 128
ATGAAAGCTG GGTGGTCTTT GGGTAAGGAC AGGGGAACTA GGAGGTAGGG
TGCAGGGTAA TGATTTGCTA CCC
C/T
TCTTTCTGGT AATACCACCA CCCTCCCTTC CTAGTTTCTT AGGAGGCCCT
TGAT

16_106 100
TCTCCTGGGG AAGAAGGAAA CTAACCTCTT CCTATCCCC TATTTAATGC T
A/G
GCATCTGCTG TCCTCTGCTG TGGTAAACAGG GAACTATCTC CCAAGGAG

16_107 141
TGTGGGGCAG CTGGAATCGG GCAGACCTGA GTGTAAACTC AAGTTGGCCA
CTGC
C/T
GGCTGTGCTG CTTCAGGCGA TTCTGTTGAC CTTTCTGTGC TACATAATGA
AAATTCTTAT TTTACTGAGT GCAGGGGCTG GGCGGG

16_108 107
GCCTCAATGA ACGACATCAG CGCTTCTCTA GTTGGTGAGA AGGCCCAGGA
AAGCTTGGTC TG
T/C
GTCATACACT CAATAGCTTC TCCTACCCAG CCACCTACCC TGCC

16_109 137
TACTTGCTG GCTGCTCATG GTTAACAGAA GCCCAGGGAG AAGCTGACTC TA
C/T
CTTCTCTTCA GCCACACCCA AGATATTGGT ATAAGGGAGG CTGGCACCAT
GAGTATTAGT ATAAGGGAGG CTTCCGGGTT GTGC

16_110 142

Table III

GAACCCTATT GTGAACTGTG CACGCAAGGG AACTAGGCTG TGCTCCTTA
C/T
GAGAATCGAA TGCCTGATGA TGGGAGGTGG AGCTGAGTTG CTGATGCTAG
TGCTGAGAGT GGCTGCAAAT ACGGATTAAC ATTAGCAGAG AG

16_111 121
CTACTGGGTT TACATTGGAG ACCGTCCCAT TTAATTTCCA GGGTG
A/G
TGGGACAAAA TGGGCTCAGT TCTTACATAG CACACTACAC ATGTTTAA
ATACAAAAC TACATTGTTG CTCCC

16_112 109
TCATCATGGT GATGGCATGC ACCTTTTTCA GGGCCGGAGC CAGTTCTTGG
AGGAGACTCT GC
A/G
CAGGGCATGG ATCACTGTGG TGCCCTTTTC CTGTGCCTGT GCCTTC

16_113 108
TTTACATTCT CTACCCTGTC ACACAATATT TCACAAGGGA ACCTGGACAA
AGGGAAT
C/T
GGTGGCAGAA GGATGCTACC CTTGCCTCTT ATGAGCTCCC ATTCACTTCA

16_114 139
GTCTCCTCAG TGACCATAAT GCTGAACAGT TGAGTTTTCT CATTGTCCCC
TATTA
C/T
ATCCTTCACC TCACAACTCT GTGGGAAGAG CAGCTGCAGG GTGCACTGAA
TATTAATCTC AAAGCAGCAG GCTGATCAGG GAA

16_115 128
TGAAAGTCTT TCCTGGGTGT CCTATAATGC AGAGAGCCAA AATGATCCTG
AAGAAGT
A/G
TCTGTCCCCA TGCCTCATCC ATAGCATCTG CCAGGCCTCA CTGAACCAGC
AGAATCTAGA CCTCAGTCTT

16_116 129
ACCCACTGCG TTCTGTTTTT TAGTCATCTA ACATACTTTG CAGACTTCTA
GTCCCATCGA TACAGAA
A/G

GGAGTCTACA AAAGAGTAAA TGTGAACCTG AGAGAAAAGT GTCCCCATCT
GGCACAGATA A

16_117 123
CAGCTAGACA CCATAACCTG GCTCACTGTC TGGCCTTCAA GTTTCACTCA
GCAGA
C/T
AAATGCACCC TTAAGTAACC TGGTAGGGAA CCTGTCACTC TACATAAAGA
ATGTATGGCA TGCCACA

16_118 141
ATCGGCGGTG CTGAGCCGTG AGGTCCCCTA CCTGCCCTGT CAGGCAAAT
A/G
CTTGTGTCAG CATACTTCTT TCATCCGTCA CTCAGCCAGA GTCTGTAAGA
CAGACTCAGC ACTAGGTCAC ATTTTGAAAG AGAAAATAGA

16_119 105

Table III

GAAGATTTTT CTTCTCCTC CCCCTGTGAC CAATAGCCAA AGACATATTT
TGGGATG

C/T

ATTAGTGCAC TGGGACCTTA CTCAGTCTAT AGATGACCAA GTTCACA

16_120 133

AAAGGAGAAA TACCAGTATC CGTCTTAAGA GCTGCTCTGA CAGCAACTCA
CAGTTCTGAT AAACACTATT TAAGTGCCTT GTGAA

A/G

GCCTTTTTTG GGGAGGCTGT CAGCGAAGCA AGTGAGACCA TGTGATG

16_121 145

CAGTAAATCC AGGGCAGATG TATGAGGTAA TGAAAGAAAA TTTAAGAATG
CACTCACACA TTGATGTGAG AACTATTAAAG ATCCCCTTCT CTCTCT

T/C

CTATACCTCA AGTTCGTTAT CATGCACTCC AAGCTACCAA ATATTCCA

16_122 141

CGGGGACAAA TTATTCACCA ATCTTCATCC CAGGCTCAGA GGAAGATTAT A
T/C

ATCCAAGTTT TCCACTATAA TTAGGTTGGA GCCATATGAC TAGGCTCTGG
ACAAAAGGAC AGTGGAAATA CTAGGCATCA CTTTTAGGC

16_123 130

TAGACAAAAG GATGAGATCT TGGTGTGGGG GGTAAAGGA TGAAGCTTTT
TCGATTCTTC TAGCATC

A/G

TGCTAGACAA ATTCCAGAAA CAAACTGGAT GCTTATGATG GAAGCAGCAG
AGGCAAAGA GG

16_124 127

GCTGGAATTA CACTGTGATG AACTAGGTTC CCACACTATT TGGTGGGAGT
GAATGAGAGG CTTTGGATGT GAATGT

A/G

GGTGTGCCTT GTTCACCTTG CTCAGGTTCC AGCAGGTGCT CAATAAATGT

16_125 119

CTCAAGTGCA CATGAAAACC TTAAAGTCAT TACAGAATTG CTAGTCCACA T
T/C

TAGCCTCACA GTTAAATTTA ATAGTTCATT TGTGAAATTA ACAGACGAAT
TTGTCTCGCC TGCTAGA

16_126 105

ATACCATAGC CACCCCGAC ACCACCACCA GATTTCCAAG ACCCCGGACC
CAGCACCC

T/C

GAAGGGTCTC TGATTCTGCA CTGGAGCAGT TTCTTCTCCC AGGCCC

16_127 136

CTACTGAATC AGAAACTCTG GCAGTGGATT TCAGTCCTCC AGGTGACTCT
AATGCAC

A/G

CTCAGGTTTG AGAAAGGATC CCTGCCCTA ATCCATCAAG CCAGGCCAGG
AGAGTGCAAT CGTAGAGTCC ATGTGTCC

16_128 139

GTTCGTTGTG TCTGGTACTC ACTCTGTGTG CTGCATCTCA CTTTCATCAT

Table III

C/T
 ATGACAAGGT GTGCAGACAA GGAAGAATGT TCCTCTGGGC TGCTTACTGA
 TAAGAATCAC ACAGTGTAAG CCTTCAAGG GAACTTAGA

16_129 131
 TTGCTATCAT GTAGCTAGAG TCGATTAAGT GGCCAAGGGT CCAAGAGACA
 GGTGAGACCA TGAGGAGGCA CATT

C/T
 GATGTGATGT GACCACAGAA CCCTGGGTAG TCTCAAGGGT AGAAGCCCTG
 ATGATG

16_130 119
 GCGGGCCATT TCATTGGCCT ACTTTTTCAT CATCGGCTAG AAAGGCCTTC
 AAAG
 A/G
 AGGCTTTGAA AACCAGCCGG CCATCTTCAC AATAAGCTCA GACGGTTAAA
 AGCCACGCTC TGGA

16_131 142
 GCTTGGATTT ACTGTGTTCA TTTCTCTGAA GCTTTTTAGA AATACCTGAG
 GAGG
 C/T
 TGGGCACGGT GGCTCACGCC TGTAATCCCA GCATTTTGGG AGGCCGAGGT
 GGTCGGATCA CCTGAGGTTG GGAGTTCGAG ACCAGCC

16_132 144
 TTCCAGATT TTGTCTGGAT TCTGCCTGCT AGAGTGCCTC ACCTTCATGA CC
 A/G
 GCTGTACCCC TTCATTCAAT TGAATGCCAC AGCTCTCTCC CCACACCCAG
 GCCTTTCTTC AGTCTCCTCA TGTCAATTCT CCTCCAGGG A

16_133 122
 AGACCCAGGT GATTTTCATA GGTATTTCAA AGGCAAAGCC AGCTCTGGA
 A/G
 ATCAAAGCCC TGCCCATCCT TCTAGGACTA GGAGAACAAG TTATTTCCAG
 ATTTCAAAC ACACATGAGT GT

16_135 138
 TGGCTGGCCT GAATATATCT GGTTCGTGC GGACAGACTC TCTTTGGCTC
 ATGTATACCT TCAATTGCAT AAGGGAGAGA ATATAGAGGA C
 A/G
 TTCCAAAGGA AGTGCTGACA GACTGCGCCC ACCTTGTGAA GGCCAA

16_136 129
 ACTGTTCCAT GGGAGAGTAT TTTAGAGACG ATGGCAAATA TACTTTG
 A/G
 TCATCTATGA CGACTTATCC AAACAGGCTG TCGCTTACTG TCAGATGTCT
 CTGTTGCTCC ACCGACCCCC CTGGTCGTAA G

16_138 147
 GGATCTCCAT GTCCCACTCC GCCAGCTTCT GGGGCGGCAT GGGGTCTGGG
 GGCTGTCCG C
 G/A
 GGGATGGCTG GGGGTCTTGC AAGAATGGGA GGCATCCAGA ACAAGAAGGA
 GACCATGCAA AGCCTGAAGT ACTGCCTGAC CTCCT

16_139 131

Table III

CAGCCTGTTA AAGGAATTCG ATACCTCCCT CCCTCCAAAC CCAAATCCAC ACCC
 A/G
 CTTCTCAGCT TACCAGGGGC ACAAATCCCA CTGGCATCCT AGAGGAGAGC
 CTCAAATCGT AGGAGGCTGG CTGGGT

16_140 133
 GAGACCACCT CCTGTCAGCT CAGGCTGAAG CTGAGAAGGG GAACCTCTGG
 ACAGAGGGAG CTC
 G/A
 GACATCCTTG ACTACAAACA TCCTGACCTG ATTCAGCAAG TGGTCTGGTT
 TCCCCTGGTG GCCCCAGAA

16_141 124
 GCTGACACTG CTCTTCCCGG CAGCAGGGCT GGGAGTCCCA GAGCAGAGAG
 GCCTCCTCTG AGTCCCTGCC GTGTCC
 A/G
 CAAGCTCATG TCTAAACAGG AGCTATGCCA AGCCCCTGGT TTCCGCA

16_142 99
 GGGTGGGCAG GGTCTGGGT ACGTCATGCC TAGGGGCAGC CTCAGCAGCC
 CA
 C/T
 CCCCCTCTG ACCTCTGAGC CCTGACCACA GGACAGCAGC GGCTTC

16_143 115
 CATCACTCAG GGACAAAGTCC CTCTGGCATC CCTTGTGGCA CCATCCATTC
 CTAGAGAAGC CAGGAA
 C/T
 GTGTGCACGT GAATGAGGGG GCAAAGCCAA GCAGAGGGCT CTCTTCTG

16_145 136
 AGAGCCAGCT GCTGCCAGAA GCTATTACTG TTATTACCGG CCGGCAGCAC
 AGGCTACAGC CACAATC
 A/G
 TAAGAGGGAA ATGGACTGAA TCCCCACACC CCAATCCCTC ACTCACTCCG
 ACCCGAGGCT GTCTACCC

16_146 137
 GGTGGCGCC AAGGTTTAGG AGCCAGCACA GAAGCCTCTG AGAGCCATAA
 GGGT
 A/G
 GAAAAGGTTA CCCGGTACTA AACCAGCCAG CCTCGGGGTG ATCTCATCCA
 CTTCCCAAGA TAAGCCCCCT CCCCACCCT CT

16_147 123
 GAAAAGGTAG CAATTCCCTC CGGGCTGAGG ATACTCCCAG TAAAAGGAAT GGTTG
 C/T
 GATTGTGGGC CCTGCTGTGT CAGGAAGTAG AATCAGATGG AAGAAGTTTG
 TTTGGGATGA CATGAAT

16_148 148
 AATTTTGGTT TGGATCTGGG TAACCTAAGA GGAAGAGAAG ACTAATCCAA
 CTGCCACACT CTTAGGCCAA GCCTGAATTG TCAGGAT
 G/A
 CCAGAGACAT AATCAGAGGG TATCGATAAC TTGAGTTACA CCAACACCAA
 TGGGTCAGAG

Table III

16_149 145
 TCAGAGACAA AGCTGAGGAA TAACAAGGAT GACTTTTCTA ACAATAGATC
 TGATGAAGTA CTGGACCAGC CAAGGGAATA TCGGACA
 G/A
 CTCCTTCCTA GACATTTGCT GAACAACTGA CTTTAGATGA AGTCCTACTC
 ATAGGTG

16_150 142
 AGCCAGACTG AACAACTGT AATTCGTCAA ACATATCAGG TGAGG
 C/T
 GTGAATGTTT TATTCGGCTC CAGGTTCTGT GCATGCTGTT CCCTCCTGGC
 AGGTTCTTGC CACCCCTCCC GCAAATACAG GTAATCTCCT CAGGTC

16_151 133
 TTCCCCGACT CCCTTGTATC TTCTCCCTGC CTTCCAACAG AGAGGGCAGC
 AGCCTCTCCC AACTGGCT
 A/G
 ATTCTACGCC TTGCCTTTGA GGGTTACTTC ATTCATAAA ACCGGTTCCT
 GCTGCCCTG TTCA

16_152 108
 TGGGGTACCC CTGGGGGAGA AATGGGGAGG CCAGACCCAG CGGTAAGCCA
 GGGGGA
 C/T
 GTGTGGAGTC AGCACCCAGT GCTGTGGGAT AGAGGGATCG AGTCTGGCCT
 G

16_153 146
 CGCGCACTCT ACGCCTTCAC CGGCCTGACC CTCACGCCAC AGCTCGAGGC
 CTGGATCCAC AACATCACCC ACGGGTCGGG GATCGGCAAG CCAATCGA
 G/A
 GCCTTCCATA CTTCGTCTAG GAATGCGCGC AACGTCTCCC AGGCCTG

16_155 145
 TCTCCAACCC TCAGTGCTGG GGGAAATGGT GCTTCATGTG TGCTGGG
 A/G
 TTGTCAGCAC TGGCTCAAAG ACTGAGTCCA CTAAGGATAC AGAGCAAAGG
 TACTCAGGAC CAGCACTAAT GAGAGATGAG AAAGCCAAGG CTGGCAG

16_156 117
 CAGGACTCAT TAGCAGGAGC TCATAAAATG AAAGTGGCAG TGAGCTCATA
 TGGAAGA
 A/G
 GCATCACGGG CAACTCGGCT TGGCTCACCA GCCCCTGAGC TGCCCCCGAG
 TGACCGCTCC AGCCTTCTT

16_157 124
 AGAGGTTCAG GGTCCCTATG GGTATCACAG GAGGAGCATA TTCAGAG
 A/G
 GGTAAAAGA GGACATGATC TTGAGGTGGA ATAACATGGG TGCCAAAAAT
 TGAGGAGTGG GGTGACTAC AGGGAG

16_158 149
 CTTAACTGTC TTCCCCTTGG CTTACCCCCA GACTCCTCTT CCACTCCTGA
 TTCAGGAGGA AGCCTGTTCC
 A/G

Table III

CCTGCATTCC CCATCGCATG GTCCAGCCAG CCTGTACCCT TCTCTGCCTC
ATCCATCACC CGTTCTGCCA GCATGGGT

16_159 141
TGGCTCCTAG AAATACTTCA GATGCCATGA GATCCACCAC CTTGAAATGT
CAAAGCAGCA AAATTCAAAC CCAGGGGCCC TGGGTGCCA
A/G
TGAGACAGCT GTTATCTTTT TTA CTCACCA GACGAGGTCA CAGATAGAAT
G

16_160 142
CTCGTCATTT GTGTGCACTA AATTTTGAGA ATCACTAGAT AATTTTCAGC
TCTGCAGGCA GTTCCTGCTT C
C/T
ATCACATGGG GCCTAGCCAA CAACTTAGAA TTGAGACAAA CAAGTATCTG
TACCTTGGGT TGCCAGGAG

16_161 116
AAGCCTTCAG GGGAGGCAGA ACTAGGAGGG CCCTGGAAGT CAGGGGGCCT
GGGATGGA
T/C
AGCCCTCTGT GGGCCCCTCC ACTGGGATTC CCAGAGGCCT TGCCCCATT
AGTGCCGGGG ATGGCC

16_162 112
CAGAAGGAGC GGGCGGGACT GGCAGAGGGC CAGCATCCTG GGAGAGAAGG
GCTGGGCTCA AAGG
C/T
GAGAAGGCAC AGATGGCACC CGTGAGCCAC GCTGGCACCT TCGTGCT

16_163 146
TGCTCCTCCT CCATAGAGGA GTTATTAAAG CCACAGAGTT AAAGTAAAT
GGCCCGAGAG CAAGACAATG AATATCAGAG AGGGTCACAG GA
C/T
ATCAAGTGGA CTTGTGACCT TGGGAGTGTA AGCACCTACA GTGGACAGAG
GGG

165 141
TGATAATGTC AACAGCTTTC GAGAGCCTCT GAGCAGTGAA TGAGATGATA C
A/G
GGTGAAAGCA GCTAGCGCCA TACCTGGCCC AGGACAGGCA GGAAAAATGT
CAGGCAGATC TGAAGCTGAA TCCGGTTACT GAGTCATCA

16_166 125
CCAGCAGGGA TTAGAGCCAG GGGCAGGTGT CATGGAAATT CCTTCCACCA
C/T
GGCCTCCACT TACTTGACTG GCCGGCTTCC TCTCTTCTGT GGGTTTAGAA
GTCACCCGCT GGACACCGCT CCTT

16_167 106
GCCCCCTCTG GGCCCTGCC TAACAGAGGG ACAGAGAGAG GGCTGTGTCC
AC
C/T
CTGCAGCTCT CTGGATTTGG CCAAACCTGG CTGCTGTGTG GCCCATTCTT
GGG

Table III

16_168 130
 GCTCACCACGAC CCTGTGAGTA CTGGCTGCGT CTCTGGGTGG CTCTCTTGTG
 TCTGGTCTAG TGTCTC
 A/G
 GGTGTGGCTG ACCCTTTGGA GGAAGCAGTG CACAGGGACA TATTGACATG
 GGTGTGGAAC AA

16_169 127
 GTGTGAGCTG GTCCAGGCCA ACGGGAAGTG GGCAGGAACG GCATGGGTCA
 CTGGAAGGCC ACAG
 C/T
 GGGAGAGTAT CCAGGGGTGT TCCTGTGTCT GTTGCCCGTG CCCGCTGGTG
 ATGGGACATC AG

16_170 122
 ATGGTTTATG TCAAACCGGA GAATGGCCCA GCCCGGCCAG GGGCTCCAGG
 ACAGTTCCCA GGTGTCGG
 C/T
 GGCTCCTACT TTCCTACTCA AGAGTAATTA GAGGGAACCC TTTTAAAACC
 ATT

16_174 132
 GGGGCCTTTC TTAGAGAAG TTGACTTCCT GGTTTTGAGT TGAATGTAAC
 TCTCCTTTGC TGG
 C/T
 TTCTCCGCTC CCACCATTCA TTTCATAAGG ACAAGGTCAT GCACATTGTA
 ATTCTACGGG TCGGATCT

16_175 144
 TTGCCGCTCA GCACAGGGCG TGAGTCAGCC CCAGTGGCCT GAGGCGTGTT
 TCAGTTTCCT GCTGA
 C/T
 TCAAGGGTCG TGAGTTTAAA ATAGACTTTG CCTGATAACT TGGAAATGAG
 GGAGATTTAG GCTGCACTTA AAATGAGT

16_176 135
 CCCTCTCCAG TGAGGGTGGG TCAGAGTAGA CCCCTGACTG GGCAGATGAG
 GAGGCTGCTC AGAGGAGGCC TCCAGC
 C/T
 CTCCCTGCCT CACCAGCCTT GCTTTCCTCC CCTCTTCCAC GGAAGCGGA
 GCTCCTAA

16_177 119
 GTTTAATGAT GCATGAGGTC TTGACAAGAA CCTAACACC AGCCTGTGGT TTG
 C/T
 TTTGGTTGTG CTGATGTCGT GGTGAGGTCA CAGCCCAGGA CCATGACCCC
 AGAGGCCCTG ATAAA

16_178 113
 CAATCTAGAA AGCGGGGCAA TGGGTAATCA GTCTCACCGT CACTAGGC
 C/T
 GAATGGGAGA AATGCTCCTG TGGACATGGC CTCCCAGTGT GGGTGAGCAA
 AAGGGCAGGC TGAG

16_179 139
 TGAAACATAC GGTGCAGGCA AACTCCAGTT TTCTTGCCCT GCAGGTGAGA CCACC
 A/G

Table III

GAAGTGCAGT ACTTAGGGCT CCAGGAGCCC CTCAGTTGCC CACAGAAGTA
GCTGGTTTAT TAACACACCC TCGATAACTT CCT

16_180 148
CCCATGAGAC ATGGAGGGCC TTTGAGAGGA AAAAGCCCAG ACCTGGCCCA
GCTCTGGGAC TCCACACGTT AGGAGGGGCT GAGGC
A/G
AGGAGCGGCC ACCCTGCCAA GCTGAGCCTT ACAGGCAGGG GCCATGTAGC
CTGCCGTCCA CCG

16_181 125
AAGGTAAGAT GACGGCAGAA CGTCACGGAG GAGCAGGGCA GGGCCC
C/T
GTTAACAGGC TGAGCCGGGC GCAGGTGAGC AGACAGCACT CGGCACAGGG
CCTGTCTAGA GCCTGCAGTC ACACCTCC

16_182 146
TTTCTTTGAG GGATGTCTCA ACGCACCAGG ACAGCACGAG ACGCCCAACC
CGAAG
C/T
GGCTGCTGCC ACCTGAGTGC GCCCTTCCAA CCTGAGGTCT AAAATGGGGA
AGAAAGCTGC ATCCCCATCC CGTCCCGGG CAGAGCCAAT

20_001 110
TAGACCT TACTATGTGC CGTCCTAGTC GCGCTTCGTA TGTGTTAAGC
CCTTT
A/G
TCCCTCACTC CAATCTGTGA CATAGGCACT CAGTACCCCG TTGCCCAAAT
GAGGAAA

20_003 144
AG CACTTTCGGA AGCCGAAGCG GGTGGATCAC TTGTCAAGAG
TTTGAGACCA GCCTGGCCA
A/G
CGCTGGTCTC CATAATACTC AGCCTATGAA GAACCAGGAG AGGGACCTGC
ACACTAGAAG ATAAATTGCT TGTGTAACT GT

20_005 146
GATTGTCTCT CTGGACACGG CTTATGTTGA CAACCTGGAT CACATTAGAG
GATCACACTG AGACCTTTAT GTCGGCCTCA GTT
C/T
CTCCATCTGT AAAGTAGAGG TTGGGCTTAG ATTATAGATG ATAAAGACAC
CAACTTTCCT GG

20_007 112
G AATACATGCT ATCTTGCTTG TAGAAGCCCA GATTCTCCT TCTTACGACT
CCCA
C/T
ACCCACTTAG GAGATTCTAT TATGTCTTAA AAGAAGTTAC ATCTCCATTA
GTGTCA

20_008 145
CAGGT GGATGGAGGC TGTTCATC TGGGGCTGTC TCTTGATTAA
GGCTGTCACC TGTTTGTATA GGGACCATGT TTCCCA
C/T
GCACTTTGAG TGCAGTTTAG GAGGTATCCT TTGGATGCTG AAGTGTGGG
ATTTTGAGGA CA

Table III

20_010 132
 ACAA GACTGCAACT TACATTCTGT AATGAAAGTT TCCATTCATT
 TGTTCACTCA ACAGTTATTG TATGCTAGGC A
 C/T
 TGTGACTGGA GTGAGGAATG CAGAGATGCT CAGGAAACGG TTTCTGCTCT
 CACCCCT

20_011 126
 GCA AGTTGGGCAT GTATCCTCGT GACCACTACA GATGTGCTAT CT
 C/T
 AATCGTGTAT GTTGAAGACT AAATGTTTTT AGTGTAATAG AACTTGACCT
 CAAATAGAAG ATTGCTTTTA

20_012 128
 TGTT TTCCATGAAT CATTTTTATG TTTTTCAAAG GTTTTACTCT
 TTTCTCTCTG GTAGTAATCA CACCAGGAC
 C/T
 CCTTTCATCT TGTACTTTGT TCTCCTCCAG TGGCAAGGTT TTGTGGTCCA
 GACC

20_013 145
 CTGTGGGA AGGGGCAGCT AAGGCAACTT GGAAGGGATG AGTATAAGGA
 AAGATATGTG GATGCTAAAG AATTGGGATG AAGAAGAAAT CTATG
 A/G
 ACCAGTTGCC CAAGTCTTTG ATAAATGAAA CGAGTGACCA AGATCTGGAT
 A

20_014 110
 TGCACACAG CTATACCTTC CTGGTTCCTG AGGATTGAGT GTCCCCTGCG
 T/C
 GCTTAAAGCT GGAGCCAGAC GTATGCAGCT TTTTCCCGCT GTCCCCAGGC
 ACCGAGTACT

20_015 138
 TCAC TGCAGTGTCT GCATGACATA TGGATAGTAC AGAGACCTTC
 AAACATATT ATGATACAGA CCAGGAAAAT TAACATAGCC
 C/T
 TAGGGCAAAA CACTGAGTAA ATATTTATGT GAATGAGGAC TGTTCCTGAT
 CTT

20_017 140
 CCCT ACCTGTGGTT
 CCTTCTGCAC CCCTGCCCTT CAGATCTGTG ATGGGCAGGA CCAAAGAGCA
 GGCCGAAGAG CTGGAACCAC GAGCACAAGG
 A/G
 CCATCTCGGC CCACTGCCCT GTGATAAAAT GTGGCCCACT GAACA

20_019 146
 AAATA AGGTAAAGCC CTTGACCTCG AAGAGTTTTT AGTAGTGGTT
 GGAGGAGTGA GGGTAGAGGG TGATA
 A/G
 CTACATATAA ATGCATTATA CTATGAAAGG TATGTGGTGA AGTTATTGTA
 TTAGTCCATT TTCACGCTGC TGATA

20_021 142
 GAAAT GAAACAGCTA GAGATGTTAT GAAGGTATAA GATAATGAGG

Table III

CATAAATCGT ACTCAAGCCC TAAGGA

C/T

ACTCAGCATG TAGGATCCAT TAACAAAGAA GGGTTACTTA CTAAAGAAGA

TGTTTTTTGG AGGGGTGCCT

20_023 126

GAG

ATCCACTGCC ATAGAAAACG TGAATGATGC TCTTCTTTTA AAGGTCAC

C/T

AAGGACCTCA CATTCTTCAA TCCAATATGT ATTTTTCAGT TGCCATGGAC

TTTACCATTG GACACCACTT ACCA

20_025 148

GGGGG TTAGGAAATG TCAATAAACG TGTCATAGCA ATTTTAGATT

TTAGCAGTGA GAAAGTATGA TTTTAGTCAA ATCTTGAAGC AGGTGA

A/G

GAAGTACTTG CCAGGTTTCA GTGGGAGCCA ATCCCAGGCA GAGGCTACAG

CAGGTG

20_026 138

CAGAGGAT TGGAACAACA GATATGGAGA GAGTACAGAG

CAGACAATGC TGTGCAGCCT TGTTTGAGGG CTGCTACAG

A/G

ATGCTATTCC ATTTGCTCTT CGGATTCAA GTTCGGGTAG AGAGTCCAGC

TAGCCAGGCT

20_028 139

TAAAGCCA TTCTGTTGCC TGCTTCTCTT TCTGTGGCTT AAACAGAG

C/T

TTGCAGTGGC CTGAAAAGTC ATCAGTCATG AGAAACAAGC TTTTCTAAAC

ACTAGGCCAG ACAGAACAGA TTAGGAAATC TCCAAACTGG AT

20_029 118

AGG GAGGAGGGTA TGGGGAAAAA TTGATGGGGA AGCCCCCAG ACTTTTGCCT

TGTGCCCCAGG ACAATGACTT

C/T

TCAGCCAAGC ACTCAAACAG TATGAAGCCA ATTTGCTGGG TTCA

20_030 136

TTT TGAATCCCAG ATAAAAAAGG AAAATACATC TGGCACTTCT

CCCTCTTTGC CATCCTGCCT TACTCTCACT TTGAATG

C/T

AGATGTGACA TCTAAAATTT CAGGAGCCAT ATCACATCCA TGAGGCAAAG

GTATA

20_031 137

AGAGGGG TTTAGAAAAG GTTGCAATGT ACAGAGGGGT TTTTAATTTG

TATTAATATT TCTCAGTTTA CTTCCCTC

C/T

ATTTAGATTT AAGATTTACT CATTAATTCA ATAAACATTT ATTGAGTGTC

TGCTATGTAC CA

20_032 146

CACCTACGG TTGCTGCAAT CTCCTGCAGC ATTTGTACTG GTTGGTATCA

TTTCTCAACT ATTGATTTCA

A/G

TTACCTTATC TAGGTCCTTA GGACAAGAAG TGAGAAATAT GATACCCAAC
TCTAAAGAAA GAGGTTTTGA AGGGAA

20_033 135
CATT CACACATTTG GGTTGGCTTG GTGGCTCCAC ATTCATTACA GGCTAG
C/T
TCCTGGGGAA CCTGGGAAAT GTAGTTTTAG CTTTTTGTCT TCTATAGTAT
AGCAATCAAA GTAAGCTAGA AGGGTGTGG AATA

20_034 144
AGGC CTTGTTCTAA GTGCTAGACT GCAGTGGGGA GAAGTCACAA AATC
A/G
CTCCCTTTT ATGTCTGTAT TCTAATATGG CAGAGGGGCA AGAGAGAGTG
AACATTGAAT TCAAGAATTA ATCCTACCTG CTACCCACCT CGACT

20_035 148
GGAT ATTCAAAATG CCTTTTGTAT
GCTCATTACA AGTTTCCAAC TGTGTTCCAG CTAGAAGGTG TGAGGTAC
A/G
TGATAGCTGT ACTACTAAGG ATTTGCCATG AAGTACAGTG ATCTATAAAA
GAATATTCCA GACAAGCAGT TCCTT

20_036 147
A CAAAGCCACA
GGTGCAAGGG ATGCAGAGAG GGACAGGGCA CAGGAAACT GCTGGGAAC
A/G
GTATGCGAGG AGGAGGTGCT TACAGGACTG CACAGAATCT CAGGGCCCAG
TGCCAAAAAA ACCCACAAGA CCCCTTGTTT CAAAT

20_037 125
TTGGCCG CTGATCCAAC AAACCAACTG TAAAAGGAAT TTCTGAAACA
ATTCAAAAGG TGTGACTACA GGTTGACT
A/G
CTAGATAATT CCAAACATGT TCATCTTGTT AGAGGACTGA TAATGAACA

20_038 113
G AGACTGTTAC AGCCACTGTA GGAGTTTCAC CTCATTCTAT CCTTTCAACA
ACCCAAT
A/G
CGATAGATGC TATTATCCTC TTTAGGATAA AATCGAGGAA ACTGAGGTAC
AGTG

20_039 135
GGTGGATT TTCTTCAAAT
TCTAGAAAGT GAATTTCTAG TAAGTTCCCC TGGCACAGCA CCA
C/T
GGTAACTTCT CTGCAAAAGA CTCACCAAGC CATGGCCATG CCCTCCCAAC
TAGGTCTGGA TCAGCCCTGG GGA

20_040 125
GAA TCCTAAACTT CCTCATCAGC
GGTGGATTCA GTTATGGGCT CCAATGTTTC ACCCCTCCGT GAA
C/T
CCATGCCCTT ACTCTTGCAA CTTTGCAGTC CCTCCCGCTA AAGACAGAAT
GAACCTCT

20_041 135

Table III

CTTAG ACCAGATATG CCTCAATTTT CTTTTCTAAG ATGGTGGCTG
TGGCCTCATA CACTTCACAG GGCTGTATAA ACTAAGCAC
C/T
AGTACGTGTG AAGTGCTAAA ACGGGTGTCC AGCACATAGT CACTGCTCAA

20_043 147
CAGAT
GGGGACAAAG AGTAAACTCT ACATCTCTAA AATCTAACTC AACATCTTTT
TCTCAAACCT GACCCTTTCT CCAGATGTTT
C/T
TGTTTCTGCT TCATTTTCAGC ATTCTTCCTT CCAGTCACGT GTGCTCAAAG
TGCCAAAGTT A

20_044 92
GTGAGTGTG GACAGTCATT TTGCTAATTC TTCTCATTGG TGGTTCC
A/G
CTAGATGGAT GATTTCCCTG AATTAGCCAT CATAACTGCC ATCTG

20_045 134
G CCATGCTTCC ACATGTGTGT ATGCTGTGTT TTCTCCTACT
TTCTGTTGTC ATCTTTGTGA AGACAGTGCC TACAACCCTC
C/T
CCTTCAAAAG ACCTACATCT TTTATCTGTG TCTGTTGGTA TATTTCCATC
AA

20_046 114
GAGAGA GAGAGGGTGC GCATCCGAGT GAGCCAGTGT TAGCCAAGAA
GCAGGGAGCA GGGCTCGAAA GTCGC
C/T
GAGCGCCGAG TGCGAGGAGC TGTGATTGT TTTCTGGTTG AA

20_047 148
CT GAGGAAGGCC TGACCTGAAA CGATTTAACT TCTATGTGCA
CACTCTGAAT TAGTTTCTGG AACACCTGAA AATGCTCCAA AGGTCCCTCT
GGAG
A/G
CCTCCATGAA ATGTTGGTTA GTTAATGGAG TGGACCTAAT ATTAGCCAGT
C

20_048 146
TAGCAAGAG CTCCAGGCTC TCGGTCTTCT GCAGCAGGGC TGCCTCCTCC
GTCAAGTGCA GCATCTTTTA GGAAAGGAGT GTTCCTAGCC TGGCAGTG
C/T
AGTTAGGTAG AAATGAATGA GATGTCAGAA ACAATATTGA CTCTGAAT

20_049 147
GAAGCCTTT TGGGAACCTG GAAGCACTTA TCCTCAGACA TGTGGCTCAT
TCTTGTTTCC TCCAGGAGCC AATAGGTGGT AGCAACGGGC CAGCAAAGAA
A/G
CACCTGCTAA GGTGGGTGGT TCAGCCTAGC TGTCAAGGCG ATAGAAG

20_050 128
CCA AAATTAGTGG GAGCTGAGTA ATGACTGTGC CTTTAACTAN
GTCATGAAAT CACTGCCCTT TCTGGCTCCT TG
A/G
CACTAAGTCT GAGAATTAGT TCCATTTACT AGGCAATGAC ACTGTTGTTT
TC

Table III

20_051 96
 GGCCCCTTGG TCCTCCATCT AAATGTTGGA GTCTGACTGC CTGCAGC
 A/G
 CACATTGGGG TCACATTCCT ATGCCTTAGA GAGAGGAGAA GCTGGGTG

20_052 119
 AGGG AAGCTGCACC CAGGGCTTCA CCCACAGGCA CCATCGCTTA
 CTCTGCCTGG CTCG
 C/T
 GGGTCGGTGA AGGGAGTGGC TGCCCTTCTG CTCAGCTCGG TCTTTGTCCC
 ATTATTTTCT

20_053 146
 GAGAAAGCC ATCTAAACAG CTATTTCAAC ACAGCGTGGT GCAGGTCATC
 ACACGACACT AAAAG
 A/G
 TGCAGACGCT AGTGCCGTGG CTCCAACCCT GGGGGTCTCC TGAGGCACAT
 CTGGGGCTTT AACACCAATG CTGCACCCAT G

20_054 127
 TTGCAGGAT AAGATTTTGG GTTTCGTTTT CAGCAATCTC AGCCTTGCGG
 T/C
 TACATGAGAT AAATATCAG AACAGACATA GATGCTTTCA AGTATTTTAT
 GCAGAACTTG ACCTGAAATT TTGAATC

20_055 93
 GAAG GGAGTCAGCG GAACTGGCTG GGGCCTGGCT CCTGCTTGGC ATTC
 A/G
 TGCCACGTGT GGCTTCCTCA GGTGGCCAGA CCACTCTGTC TGAG

20_056 136
 TTGG TCATGAAGAC ATTTAATGGA TTCTCTGAAG TGGTGGCAAG
 GTGGCAAG
 A/G
 AGAGTCCAAC CTGAAGCTGC AGAGCCTGGG ATTGCGCTGC ATGGAGAAGA
 AAGGGTGTGC GTGATTCCAC GCTCCTTTTC ATC

20_057 127
 GCAAA GACCCCTCTG CACCGGCGAG CCAGCACCCC ACTGCCCTG
 TCCCCACGGG GCC
 A/G
 CCAGCCTGGC CGCCTGAGCA CAGTGCCTTC CACTCAATCC CAGCATCCCC
 GGCTGGGCCA ATCAGCCT

20_059 147
 C TCTCTCTCTC ATGCATGCTC ACTTTCTTCA ATGAGTTGTT GCACATTTAT TGAGCATCTA
 CTATGTGCTG GCACTGTGCT AGGGACATAG ATAAC
 C/T
 AAGGCAGGGC TCCTTTACAC CAGGCCTTGT TAGCTAGGAA AAGGGACCAG

20_060 110
 TGATGCCTT CATGCTGCAT CTTTGGGAAG GGAGGAGCAT TGTGTCCTCA
 CAGAGCAGAA AAT
 A/G
 GAAGGGCCAC AGGACAAACT CCCTCTATCA AGCCTTTTCA TAAGGGC

20_061 132
 CATCG CATTGCCGGT GCACTCACAC ATACCCACAG TTACTCAGAC
 TGGGACCACA CAGACATGTC AATCGACCTC ACATGC
 A/G
 CAGCCTTGGG AAGTGAGAGG AAAGTGGAGC ATCCAGAGAA TATCCATGCA

20_062 125
 ACACCAT TCCCACACCA GCTTACACCC CTGGCACGTG CACCCAGAGC
 CCCAGTTCT TCATCAGGCC AGTCATCGTG
 A/G
 TCATTGTTAT CTACTAACAT CACCTGAATT TCTCAGGAGC TTACTG

20_063 143
 CACTGC ACCCAGCCGG TTATGCGATT TTTATCAGAC CTTAGATATC
 TCTTATATAG ACAGGCAGAT TATGTAGTTA CAGACAGTAC CTCAGAAGTT
 C/T
 GATGTCTGTG ATCAGTTTGT CTTTCGAAAT CTTGCTCACG AATGAG

20_064 125
 TGGAAG GCTCTTAGGA CTGCTTGAGT GTCTTCACAA CATGGTAGCT
 G/A
 GCTTCCTTGA GAACAAGTGA TCCAAGACAG CCAGCAGCAT CTTTGGATTG
 ATTTTCTTGT CAGCAGTGGG GTGTAGTG

20_065 145
 CAA GAACACAGCT TCAAAAAGGT CGCACATAGA GTGGTCAAGG
 AGGAAGGGGA CACC
 C/T
 GCCTACCCAG CCAGATCAGC CGAATCAACC CTGGTGATCA ATGGGGTGAC
 AGATGTCGCA GCTAGATCGT CCTCACATCC AAAATAA

20_066 130
 ACATTC CCAATGACCA TATAATAGAG AAGGAGAAAC AGTTTCTACA
 TTCCCATATG GTATCTTAAA GATTTAAC
 A/G
 TTTCAAAGAT CAAGAAAGTT TACTTTCTTT CAGATTAAAT AATGAGAAAG
 GCAGC

20_067 129
 AGGCTG CAGATGAAGA GATGCATAGG GTGAGGTATG GGAAGGGGTG
 CAGAGCTTCT GCGTCCTCCC TGGGCCT
 A/G
 CCACCTTCTA GGAACCCAG CATGTCTGGC TATCAGGAAG CTCTC

20_068 142
 CAGACAC CTCAGGGCTG CATTAAATGG AGGGACGGCT CTTGTTATAG-A
 C/T
 GAGGAAGTCT GAGATGTCGT GCCATACATT GCTGTCCTCA TAGAGGTAGG
 TCATGGAGGA CTGCAGCGAG GGCTGCAGGG TGGATCGGTG ATAC

20_069 105
 GCCGCGTG TCATGAAATT CGAACAAGAA GTACTGAATT GAAGTGGGGA
 TGAGAGGT
 C/T
 AGATGTGAAG GGCTCCTGCC AGCTTACCCA GGTCTCTTGC TCAGAAGA

20_070 116

Table III

CAGAAGCAG GAGCTCAGGG CAGATAGAGG CCTGGAGTGG GCTCTGCATA TGTTCC
 A/G
 GAGGTGAGGA TGCAACAGGA GAGTGTCTG CTGTCAGGAT TAGAACCCCA
 AGAAAGGGGT

20_071 103
 TTGGGATCTG GTTGGTGGTC TCAGGGATAA AGAGGTCAGG AGTCATCCAT T
 C/T
 CTGATTGCTT CCTGTCTCAG CCTCACATCC AGCCCAACAG AAAGCCCTGT
 T

20_072 128
 GGGGA AAGAAGGCCA GGACACGCAG CCTGGCATCA CCGTGCCACA
 T/C
 GATGTCCCCA CTCCAGACAA CACAGAGGCT GCCTGGCCCT GGAGACTCAC
 CACGTCCTGC TCCTCTGGTT GGAATAATG AG

20_073 123
 CG AGGTCCGTGC GTTGCCGCTC GGCCGCCATG TAAAAGTGGG TCAGCT
 C/T
 AGCCTGGAAG GCCCGCTGGG TAGAGGCAAA GGCTGCCAGC TCTGGGAACT
 CTGCACGTTT TGCCTCCCCA GCCCCT

20_074 120
 A CACCCTGCTG CAGACTGGCT TCCCCTGCCG TGGGTGAGGC AGGACAGGGG
 CACACCAG
 C/T
 GGGAGGGCTG AGAACTCTTT ATGACAACCT TCCATCTAGA GAGAACTCTT
 TTAATTGCCA

20_075 108
 G AGATCAGATT AATGCCATGA TTACTGCTCT GTGCACCTTG TATGTCCTCA AAGAGATGA
 C/T
 CCCACATTTT TGTGAATGTC CAATCTGATG TGTGAGCCGT CTTTGAC

20_076 116
 GTTCCACTG CAGAGACGAA TCGGTTTATT CACAATGATG AACTCATCCT
 CTACTGACGA ACA
 C/T
 CTGAACCTTT TCCTGTGTTT TGCTATTATA ATTAGTGTTG CAACGCATGG
 CCT

20_077 131
 TGGGAGGAA ATGTTTATAA AGCATATATT TGATGAAAGA TTTGTATTCA
 GATTACATAA AGAACTCTCA G
 G/A
 ACTCAATAAT AGCCTTTCCT TTTGGTGGTG CACAGCAGCA ATATGGTGGT
 GAAAATTTCT

20_078 115
 GGACCTTGGG TGCAGATCAA AACTAAGCT CCATGTCCAG CCAGGTAGGC
 CCCACACTC
 C/T
 ATTCTTAGAG CAGAAGAACT AATTCAGCT CTACCTTCCA TGGCTGGAGT
 CTGCT

20_079 109

Table III

GGCCATGGCA TGTGTTTACA AAGTTATTTT GGAGATAAAG TGAGACAATG A
A/G
CAGAAAAGGC CGAATGCAGT GCTCACCCAC TATTTTTTTT TCTCCAAACA
TAAGCAT

20_080 137
GGATCTAGA ACAGCCCCTA GTCCCACCGC AGAGTGGACT TGGT
C/T
TCCTGGCCAA TTGCAGGCAA TGAAACTCTT CTTTCTTCAT CCTTTCTACA
TGTGGAATCA AACCTAGAAA TACCCTTAGG AAGGAGTGGA TGA

20_081 111
TAAC CCTAAACTGA ATCCTCTCTA GAGTACAGTA TATCCCAGGG
CTCACTTGGG GTTCTGTTT
C/T
CATCTCTCCA GAGCATTATC TCAAACCTAC CCAGACTCGC CCACTAT

20_082 101
CATTTG GTAGATGGGT CTGTAGCTGC TTTGGAGAGG GCACCC
A/G
CAAGCCAAAT AGAGAAGGGA TAGGGTGCTT GCCAGGCTGT CCCCTAGAAG
GAAAAGGT

20_083 131
TCCAGGCTT GTAAATACGT GGGCCCCTGA ATTATCTGTT GTGAGGCTGT
TATCTAGAAG CAGGGGTTTG GGGTTTGAAG CTAGG
A/G

TCGAGAACCA TCAGAATACA AAGTACTGGA GAAAGAACAT TCCAG

20_084 133
CATCC TTCAGTGA CTGATAGT AGAGGGAGAG TGACCAACTG
GCTTGCCACT TGCTCAGTCT GCCCAGGACT GA
C/T
GGGTTGCCCG GTACGTGGGA CTTTCAGTGC TAAAACCAGT AATGTTCTGG
GAAAA

20_085 143
TGG TCTCATGTCT CCGGAATAAG TACTCAATAG CCACAGCTGA
GGTGCCTCAT G
C/T
ATCATGGGCA GCCACAGCCC CTGCCCCAGT CCCCTTGTCT GATGAACACA
CATCATGATG CCACTCTATA AAGAGGACCG TTGCCAGA

20_087 127
TGGCCCTGAG AGTTGGAACT GAAGCCCATG TATAAAGACT GG
A/G
GGGCCGGGTG TGGTGGCTCA CACCTGTAAT CCCAGCACTT TGAGATGCTG
AGGTGGGAAG ATAGCTTGAG CCCA

20_088 137
T CTTGGCCTTG CCTGAGATTC TAACTGGAAC ATGGAGACGA
TGTGTATATA GGGAGGGA
A/G
GAGAAAAGCA TGAGTGGCTC TCTCACCCAC TGATTGCTAT ATTTGATCCT
CACTTAGTCT TGGGAGATGG AGCTCCT

20_089 141
 TGGT AGCCAGTGCA TGGTGAGCCT GTTTCACCAC TTTATTAGTC
 TGTTTTTCATA CTGCTGATAA AGACA
 C/T
 AGCCAAGACT GGGCAATTTA CAAAGGAAAG AGATTTAATT GGACTAACAG
 TTCCACGTGG CTGGAGAAAC C

20_090 149
 CCACTGTT CCCATATTCT CGTTATATTC CACAATGACA CATGGCCTCT
 TAGTTTTATT TCCATTTCTG TGGTCTACCT CAATAACAGT AT
 C/T
 GTTGTGGAAT GTTGAAAACA TTGTCACCTC CTTGTCAGAC CATTTTGGTG
 CCATAAAT

20_091 118
 G AGATCAGACC TAACCAACTC TATCTTGCCT CTACCCTTTA AGCTGTCCTT
 GTTCATTCCCT GGGTGTA
 A/G
 GCAGAACTAA CCTTAGGAAG GAATTTAGTT TATGGTTTGA CTGAAACAA

20_092 134
 GTC TGGTACAGTT TTCCAGAGGT TACATGATGT GTGATGATAT
 CATCACTCTG ATAGCTAATG GAAAGTATGA
 T/C
 TGTATATTCT GTAATGTTCC AGGAGTTTCT GAGGTTTAGG TTTAGGTTAT
 AAAAGGGGGC

20_093 138
 TCCACA AAAAATGGGA AGACTCCCCA TTAGGGAGCC TGATGAGGGG
 TCTGTGAGCT GGTGCTGAGC CTGGAATGGG G
 A/G
 ATGCCATGGG TTGAGTTGTG TCCCCCTAAA ATTCATATGT TGAATTCCTG
 AAGTAGTTGT

20_094 133
 AGTGCTG CAGTGAGCAG GCTTATCCAG CCATCTTTGC ACACATGAAT
 GTTTCTGAGG ACATCTTTCT AC
 A/G
 GGTGATATTG CTGGGTTGTA GGTGACAAGC ACTTTGAAAC TCGACTCCTC
 AGCCAACTA CCC

20_096 131
 C GAAACTAAAC TTCACATGGA GCTCCCAAAG ATTTTCATAA
 TCTGACTATT AATTTTCATT TC
 A/G
 ACCACCATCT TTCTAATTCT ATGTGTGTAT CTTATTTATA TGTCAGTTGC
 TTGATAGTCT AGACCCT

20_097 149
 ATCTCCAT CCTGAGCATA ATTAATAATA CCTGAATCAG ATGTTTGATG
 TGAAGACTGT ATTACTTTAT GAATGATGTT TCCCAAACAG TGGCA
 C/T
 ATAGAAGGCA TCTTTATGTG TATTTTAGGA GCATTAGCTT ACAAAGCGGG
 GAGCC

20_098 127
 TGATGA GGGAATACAT TCATTCAACA AATATCTATT GAGTGCCTCT

Table III

TTCACACCAG CTACCGGGCT AGGTAGCTGA ATG
 C/T
 TTGTCTGAAT GTTTGTGGTC TGAATGTTTG TGTTCTGCA AACTCA

 20_099 125
 CCAG GGCCTGGACC CCGTTACCCT ACAGACCTCA CTACCCAGCC
 CTCCTCTCA CTCCTGCTC CAGCCCCATC AGCTTC

 C/T
 TTCTGCTCTT CCAATGCGCC AGACACGGTC CCACTTCAGG GCCTC

 20_101 120
 CTGG ATGGAGTTGA GTCAAACCTGC CTCTGGCCGC CTCCAGCTTC
 CTGCTGGGCT TTGCT
 A/G
 TTAGGGGCAC CAAAGAAGAT CAGAGGGTGC GAGAGAAAGG GTTTGCAAAT
 TTGCAAATAT

 20_102 106
 TCTGAGCAAC TGGACTATCT TTCCAGAGTC CAGGGATTCC AGGTAA
 C/T
 TGTCTGGCCT GAGCTGTGAT GGCTGTGCCT CAGGACAGTC ATCTTTTGGC
 TTCTCTCAG
 20_103 126
 GC CGTTGTTTAT CGCCCTCCCG TGGATTAATC CCCTGTCAGT
 TAGGCCAGAG AAGCTCTGGA GAAGGCCTGC
 A/G
 TAGCATCCCA TGTGTCAAGG CCCCCTTTGA TACACTTTAT CTGCCCTTAT
 CCC

 20_104 148
 CACATG GCACAGAAGT GCTTATAGTT AGGAAACAAA GGCTGGAATT
 TCTTTATGCT CTGACA
 A/G
 CCAGGAGGTG CTGCCCAAGA CTCTGAAATG ATTCCTGAGC CAGCCCCCAG
 GCCCTGTCAG TAGAGTTTGA GTCTAAACCA AAGTG

 20_105 120
 CTTGCCCTG CCCCCACCAC CTTATGTCTG TGCCTCCAAC ACATCAGGC
 A/G
 TGGTCCTCCG GGCCTTTGCA TGGGCTGTTC CTTCCACTTT GCCCAAATGT
 CGCTTTCTCA GGGAGGCTT

 20_106 124
 CCACTCTC AAACAGAAAG TTCGGAAGGG AGGCAGGTAA GTGTTAGAAA
 GCGGTTAATG TCATGTT
 C/T
 CTATCAAACCT GAGACTGCCG CCTAGATGCC ATCAGAATGA TTGACAGAGA
 ATGAAATG

 20_107 147
 CCCTTC TCAGAGGGCT ATGTAAACAT TTAATAAGTT ACTGTAGTAA
 GTTGCTTGA GGAGTGCCCTC ACCCATGCAC TCAATAC
 C/T
 ACATTCGACA AAGTGATACT GAGGCTTTTC TGTGCCAGGA ACGAGGATAA
 AGATGGTGAA AAA

Table III

20_109 111
GGAGT TCCTTTGTGT GAACCTAAAG GATTGATTGA GATGATAAAA T
A/G
TCATCGCTGC TCTGACTACG TCTTTGATAT TTGTATGGAA TAATTACATG
AATAGGTCCA ATGG

20_110 128
AGTGCA CGGATTCTAT TAGGGAAATG CGGTGGTAAT TAATGAATCC
TGCCAGTAAT
C/T
GGGAAGGTGT GAGTCCCCGT AATATCGTAA TGATAGTCAT CTGTCTGCGA
ACCCCCATC ACTCTGAGAG A

20_114 137
CCAAT TTAATTACTT CTTGCTTCTT CTATTATAAG ACACTTATTT
CCTGGACTGA GAGCCATCTT CAACTCTATC AGCTACTACT
A/G
GCTTTTCTCA AGTGACCCAT TCAGCTGTCT CTTCTACCCA CAGTAATGCT
C

20_115 143
AGGTGG CACCTGGCTG TGATCACTGA AAGCACTCTC ACCAGCTGGG
CTTTCAGCCA AGGTCAGGAC TTTGCACCAC CC
C/T
TTCACACATG CCCCAAGGCC ATGTCCCAGC AATGCCCTCA GGACCACTGT
AAAGGAAGCA CAGTG

20_116 139
TGA TTCTGAAGTG CTGTGAGGGT CTGAACAGTG GCTGAGGTTT
ATTTTATAGA ATTTATACGC CTTAAAG
A/G
CTGAAGTCAG AAATTTGGGA TTCCATTCCC ACATGGCCAT CTAATACAGG
TATGATCTTG AGAGGTCA

20_118 128
CTGGA TGACTTTTTG GCACCGCCTT AAATTCTGTG GCTGAGGCAA
GTACCTCC
C/T
TCGTCATACC CTAATCCTGA CTCTGCACTA AGTACTCAGC ACCCTACAGC
GATTGAGGCC ATTGCTGTTG TTTT

20_119 125
GCCACATGG TGATGCGTGC AGTTAAACAG GAAGCTGGCG GAATGAGTGC
CTGCGTGGGG A

C/T
GGAACAGTTC CGCGTCTCGA GTACAGTGGT GGGGAGATGT GTCTGTGTGT
GTGATAAAGC TTC

20_120 136
GATCATG AAAAGTTTTA AGGAAACTCA GAGAAAAAGA GAACAACGCA
GCTTAAAACT TTTAAATGT CCTCCCTCAC CCGTGGCTCA
G/A
ACAGCCCTGC ATCTGCCGTG GCCGGCACGT TTCTGGTTGA ACTGCCTT

20_122 128
T AAATACAGCC GGAATGATCA ATACACGTGT CCTAAGATCT

Table III

AAGGAGAAGA GCTGTAAGTC ATAA
 C/T
 GTATGTCCTC AGTGTGGTGC TCCCTCTCCC ATGTTCAATA CTGAGTGTAA
 ACTTTTTTTC CA

20_123 101
 ATGAGCA CTCTGCCTTG GTCCCTGGAA GCCTTCCCTG CCATGAGGTT
 GGAGTCAC
 A/G
 TGGTTCTTCG GTGGGACCCT TAGAATTAGG ATTTAGTGAG CCCAG

20_124 119
 TGTCC ATCATCTCAG AAAGTGCTAC TGGGTAGTAC CGAGGGTCAG GGTG
 A/G
 CTGCACATCT ACTTTGCTGT GAAACAAGGG CAGATGTAGT TTGGATTGGC
 TAGCCTTCCA GAGTTCTCC

20_125 147
 CTAAGCGG TCCTCCCTTT TCGGCCTCCC AAAATTCTGG
 GATTA
 C/T
 AGGCGTAAGT CACCATGTTT ATCCAAGAAA TAAATTTTGT GTTGTTTATT
 TGGACTAAGA TATCATCTTA TTTTATCCTA TGAAGGATCT GTTGTAAGCT TC

20_128 120
 AGCGGAGCTG TGGAGAAAGG GCGCAGTGAG CAGAGGGGAC TTGGGCGGT
 A/G
 AGAATGAAAG AGGGGACGAG GGAGGTTGGG GGTATATGAA TGGAAAAGAG
 TAACGTCGGG GGCAGGACAA

20_129 101
 AA CCACTCTCTC TCCTCTCAAG GGTAGCTCAA GCACTCTCTC
 TTTTCATCAC TCATCT
 C/T
 GTCTTACTTC ACTACCACTA GTGTTCTAT CTACCTGGAC TC

20_130 146
 CC GGAAAGCTTT GGGCAGCTTG AACAGCTTCC TCCCACCACT
 CTGCACTCCC TGAGCCCAGC AGCCTGCTTC CTGTGAACTT TCTAGAGCAA
 ACGGCCCC
 C/T
 GTGCAGAAGC AGCATCCACG GCTGAGCAAA CAGGTGGTCA CATGG

20_131 143
 GGCCACAGG CAGTACTGAT AACGCCAAGG TTGCAGTCAG CTAACATCCA
 TTCTCCTATC AGCCAAGGGT CTGGC
 A/G
 ATAGCCGGGC ACAGGAAGAT TGTGAGTTAT TTCTTCAGGA GGGCTGTGTG
 TCCTGGACAG TGAAGAAG

20_132 143
 CATCAGC CAGGATTGCC GTTACAGTCT TTTTCTCAGG AGCTACAAAG
 ATCTCTTCTT GTTACTAAAT
 G/A
 GTCGCACCCC AGCAGCCTCT CTCGCACACC GGGGCCCTGC ATGTCAGATG
 GCGTGGTCTG CAGGGGGAGC TCTGT

Table III

22_001 127
 AT GCAGATGAAG CCTTCAGGTA GCAGGCTTCC AAGATAACAG
 GTTGTAAATA GTTCTTATCA GACTTAAGTT CTGTGGAGAC
 A/G
 TAAAATGAGG CATATCTGAC CTCCACTTCC AAAAACATCT GAGA

22_003 147
 TCT TTCAAAAATG GAAGGGAAAT AAAGACTTTC TCATGTGCAC
 AAAAGCTGAA AGAGTTCATC
 G/A
 CCACTATAACC TGCCTTATAA GAAATGCTAA AGGGAGTCCA TCATGTTGAA
 ATAAAAGAAT GCTAGGCAGC AACATCAAAA CAT

22_004 148
 CC CTCCTCCTGC TTGGCTCTGT AGCTGTCATT GTCCAAGCTT GGAGGGCTC
 A/G
 TGTACAAGCT AACATGGAGG AGGAGCTGGA AGATTGCCTC TCCCGGGGGT
 CTTGCCTGTT CAGTGGAAAG AAGATGGGAT CATTACAGCC ACTCCA

22_005 147
 A CACTCACCCCT TGCTCTGCTA ATAAGAGGAA GTAGGCGGGG
 ACGTGGTCAT CACCCTGAGG
 T/C
 CCCCCAACCCA GCTCCTCACA GTGGGAATAA ATGAGCACAG CTCTACAGTG
 GAGCCAGCAG TCTCGTGACA AGTCTGACAG CAAAG

22_006 149
 TC AAGTGTCCCA CCTGCCTTGG CCTCTGAAAG TGCTGGGATT
 ACAGGCGTGA
 A/G
 CCACCATGCC TGCTGGTCTC TGCTTTTTGA ATGCTGACAT GCTGACCTTA
 GATGTGGGGT AGGGATGATC AGACCAAGTA TTCTGAATTA TGGACT

22_007 140
 AGCCG GTTGACTTCC
 TAGGGCCTTG AGTCACATAC CACCACTCCA GCGCTGGGTG ACTGC
 A/G
 GGTGGGTCAT CATGCAGCCT CATTCATTCC CCTCACTGGC CTCCAAGGGC
 TGCTTTGAGA AACCCCTCAC GCAGCACAG

22_008 143
 CCCCC AGGCTGACTC AGAGACGTGT CCCTCCACCC GTGTGGCCAT
 GTGTTGTTCC ATCCTAAAGC TATGGCACAC TCCCATCAT
 A/G
 TCCCTCAGTG CAAACCCACC GAGCCCTGTG GTAGGGACGC AGTGTCTAGG
 AAGGCCTC

22_015 110
 T TGGAACCTTA TTACACTTCG AGTCACTGGT TTGCCTGTAT TGTGAAACCA
 A/G
 CTGGATCCTG AGATCCCCAA GACAGAAATC ATGATGAGTA TGTTTTTGGC
 CCATGACA

22_016 149
 CCCAAATGT CAGGGTCCTG GCACCACAAG GCCTTCCAAG AATAGGAGCC
 CAGAAGTCCT CATG
 C/T
 GCAGTTATAG CAGGTGGAAA TCTACTTTTT TATTGAGGTA CAACTAGCAT

Table III

ACAGTAAAGT GCATAAATCT TAAGTGCATA GCTTG

22_018 129
TC ACTGATGGTC ATGCTGGTCT CTTGTTTGTT GAGCAGCAAC
ATAAAGAAAT TGTCACAGTG AAGAAACAG
C/T
CACTTTTGGT CAGCCAGGGC AGATGGAAAA AGGGCCTAAC GGGTACACAA
CGTGAAC

22_019 132
TCACAGGACG TCTCCTTCAC AGTGGGTCTG TGCTTCTTTG TGGCCCAGAA
CAAATTAGTG GGGCTTGGAT TTATGAG
A/G
CAGATTCCCC AACCTCTGGA AGGTGTGACT TGCCACAGGG AAAGAAGGCC
CCTC

22_020 141
TCAAGTGA TCCTCCTGCC TCAACCTCCC AAAGTGCTGG GATTACAGGC
ATGA
A/G
CCAGTGCACT TGACCTGATA ATAGGATTCT TTACACTTTA TTATCAGAGT
GATCTTGAAC CCTTCTGGAA TTGCATAATG TCAGCCCC

22_021 144
GAACT CCAAACCTCCT TTCTATTCTT TGTCAGGCAG AAAGCGATTG
G/A
CCTGGGCTGG TTAGCCTGGT TCTCATCTCC ATGCTCAAAA GCTATGTCAG
GCTCCTGGGA AGGGATGCTA TTGATACCTG GCTACTTGCC TAGCTGCT

22_023 132
GTGC AGGGCAGAGT CTCAACACAG GAATTGGAAC ATAACAAATC
T/C
GCCGACTGCC AGCTTTGATC TCACAAGGAT GGAGTTGGGG AGGTGAAGAG
AAAGTAAATG CTCTCTCGAC TTTCCAAAGG AAAACAA

22_024 124
GGAGAGGGA TGCGGCAAGA GTTAGGAAGT GTCTAGATCC TTGGTTCATT
TATCAACAAA TGTGAGCCAA ACCA
C/T
GTGGTGGGTG CTAGAATACA CCAGCGATAA GAACTGGGAG AACACTGCCT

22_025 106
CAATC TTTTCTTTTC TTTCAACAAT CTGTTTCATGC CACAACACT GACTA
C/T
ATATCTAGCA CGTATAGGTA CTGTGCTAGA AAGAGAAGCT GGAAGGTGGG
AATAC

22_026 102
TATGTGGT AGGGTGTTAC GTTGGTCAGT TTTTAAGGAT AGTCTACAAG
ACCATACG
A/G
TCTAATGGAA AGAGAGAGCT AGACTGAGAG GTATAATGGC ATTC

22_027 127
GA GCTGTTTGCT ATGGTGGCAG TAGCTGGAGA GCTACTGTTA
ATTAATTTGA GCAACAGTGC
A/G

Table III

GCTGATAAAT TTGATCTAGC AGGGAGGTCT GGGACTGCCA TCCTGAACTC
AAGGTTCTCA AATC

22_028 120
AGTAAGGG TAACCTGTCA CTCCTTCACC TACCATGTAA TCCTCATGGG
CAA
C/T
TGTCACCCAT TTCACCAGGC GAGAGACAAC CTTGGCAGGG AAGAGGTACT
GGCAATCACT GGTAACCTG

22_029 127
C GGGGTTTCTC CATGTTGGTC AGGCTGGTCT CAGGTGATAC GCCC
A/G
CCTTGGCCAC CCGGAGTGCT TGGATTTATA GCGTGAGCC ACAGCTCCTG
GCCTAGATTA TAGGTTTTAA CATGTGACCC C

22_030 110
TGG CTGAGTTAGA
GTGGTGTAGC ATTGAGCTGC TCAGTTCGTG GCAAGGGTGG GATCACGGCT
A/G
AGGCTGCAGA CAGCACCACA GTCTCCCGCT GCGAGGGTCG GTTGGT

22_031 105
CT GCCTCTTCCC AAGACTCAGC CACACAAGAC TACTTCCTTC AGGAGA
C/T
GTTGGTTTTAT GTGCTTAGGG TCTCTGCATG AGAAGTTCCC TGCTTGGGAC
GTCCCT

22_032 124
CA TGGCAGAAAT CAGCAGCTTC CCCTGGGGAT TGTCTACTGA
GCACCTACAG AACCATATGG G
C/T
CTACCAGGAC TGGGACAGTG GCCCAAACA TAGAGGTTCC TGATCGGCTC
AGGAACTAGG

22_033 128
CT GGAGATAAAG CCTCAGATTT TATGACTTAC ATGTGATGAC TGAATGTTCA
T/C
GTCCCCATTT GTGTTTCCTA GGGCTGTTAT CACAGATCAC AGCTACAGTA
AATGTTTACA GCAATTCTGC TGTCC

22_034 121
TTAG TATGTCTCCT TCCATCTCAG GCTGTGACAA CCAAAAATGT
CTTCAGACAT TGCCA
A/G
ATGTCCTTAG CTGAGAATCA CTAGTTGAGA ACCACTGCTT TAGAATGTAA
GCGCCTTGAG G

22_036 124
TGA TGGGGTGTTT GGAGTTGACA AAGTATCGTA AACACTCATG
TTAGCGCCTT TGATCTCCA
C/T
GAAAGCCTTA AAAGACGGGC AGGATTTCTT CCTTTTTTAT AGGTGAGCAA
ACAAGGGCAA

22_037 136
CA AGATGTAGAG GCACGTGCTT AGGGTCACCC AGCTCAGGCC TGGTAGGAGC

AGAACC

A/G

GAACCCAGGC CTGCTTCTTT GTTTTATTCA AATCCTATGC ACAACTCAGA
CAGTTCTACA ATGAATTCAA GCCTGAA

22_038

124

AG CACCGCAATA CTGACAGTCA ATCTGGTAAT GGATTGGCT
GCAAAGTGAC TAACTCAGGT AGCATGTACA G

C/T

ATGGATCTAC GGGACAAATG GGATGATCCA CATTCCAGGG TGGACAGAGT

22_039

141

TGGA GAATTGGGGA CCTTTTAACA ATTTTCTACA AGAACAGTGC CGC

C/T

GGTGATGTTG CAGAAGAGAG CTTAGACTTC ATCTATGAAG CCACAGAGCA
TGGTGTGGAA ATCTGCAGTT AGAAGATGGA TTTTGTGCGA CAG

22_040

147

TTTG GGAACGTGTCG CCAAGCGGGG AGGAAGGGTA TGGAGCAGAT
CCATGGTGAT CACTGATGCC ACTTTACTCC CTTTCCATTG CC

A/G

GAGGAGAGAA ACCATTTTGG AGCTATAGTG ACCTCATTTG ATGGAAAATA
ATATTTGGCC

22_041

148

CAGCCCTGA CTGCAACCTC TCTGACCACA GCTCAGAGAG GGCATGTGGC
ATGCTCACAA ACAGTCTGTT AGGGGCTTCC

C/T

CTGGGTCAGA ACTCAGACCC CTCGGCTCTT AGTCCAATGC TCCTCTCCTA
ACCCAGGTTG CCTTTGGG

22_042

128

CCC AAATAACCCT ATGAAATAGT TATTATTATT TACATTTACA
GGTGAGAAAA CTGAAGGCTA CAGAATTAAA AGACA

C/T

GAAAACAAAG CTCAAAGAGT GAAATGACTT GCCCAAGGGC ATGGGAAGC

22_043

111

AGGGCTTTG CCACCTGGTT GAGGAGACAG ATACTTGAAA ACAGAGAAGC
ACAAG

A/G

AAGTGTCTGG ATCTTTGCCG ACATCTGAAC TGGCAGAGGC TGCAAATGTC
TGAGGG

22_044

126

GGGGGGA GGCAGCCATG CTCTGAGCAC CTGCTCCTCA CCAGGCATT

C/T

ACCAGGCACC ATCTCACTTA ATCCTTCCAA GAATCCTAGG CATTACGGGA
CTTTCCATTG AGGCTCAGAG AGGTCCAGT

22_045

147

TCCTGAGCC AACTTTAAAC ATCTTAAAG CACTATCACT ATTCCCACTT
TGCAGATGAG GAAACTGAGG CCTCACAAC TGTAC

A/G

CAGTGGCTTC CAGCCTCCAC GGCCCCAGGC TCCGTTCAAG AGCTGCTGTG
GGATCCTGTT TC

Table III

22_046 110
 TTTTA AGTCCCTACA TTTTGGGTTA ATTTATTACG CAGTGATAGA
 TAACTAATAT ACCTTGCCAA
 G/A
 CAATTGTTAT TGGAAGGCTG GTAGACGGAA TAATATTCCT GAAG

22_047 144
 AGGTGTGCAC TGTCAACCCTC AAGCGGCCTG AGAAGAGGTG GTGCAGCCAG
 CAGGGGCCAG TCCTG
 C/T
 GTTCTTATCC CCCTCTTGTC ACAGATGCCT GCAGAGTGGC TGGTGATGGG
 GCCTGCGCTT GCTTGCTAAC CAGTCTCT

22_048 104
 TGGAAGGC ACAGTCCAGT GAACAGACAG CCATGTGAAC AAA
 C/T
 AGATATAGAA TAATTCATTC TACCAATGCT ATGGTAGAGG TGTGGGCAAG
 ATTCTGGCTC TT

22_050 133
 CCCTGC CACTTACTTG CCATATGACT TTGGGCAAAG GACTGAACCC C
 C/T
 GCTGAGCACC AGCTTCCTCA CTTATAAAAT GGAGATTAGG ATATTATGGC
 AATAGTACCT ACCACATAGG ATTATTTTGA GAACT

22_051 128
 TTTCCATT TCAATTATCC CTTTCTAAAA CTGGGTCTTA AGCAAACCTGG AATTG
 A/G
 GTGTTTCCCA GGTCTCTTCA AACACTTTAA TATGTTGGTT CCCAGACTTC
 GGTTTCAGGG AACTGTAAGG TTGA

22_052 132
 T GAATTATAGA CTTGAACCCT GGA CTCTCAC ATTAAAAATC TGATGCT
 C/T
 GACCAACTGA GCTACACAGA CTTCTAACCA GACTTTTTAT CCCTTTCACA
 GCAGCATCCC CACATCCCAT GAGTTAATTC TGT

22_057 149
 CATGACA GAGACCAGCT CTTGTTTCAGT GCCCCCTACC TGCTGGCTGC
 TTCCTCGGCT CCTCGAACAG ATCAGCCGAG CTTATGGAGG AACTTGC
 C/T
 GACAGCCTCT CTAGGCGGGC CCTGGTCTCA TACTAGAGAA GACAAGGAAA
 AGGA

22_059 143
 GGTGGCC CAGCGGGGCA AGAGAGTAAG GACTGGGAGC GAGTGGGACC
 A/G
 AGACAAGAGG CCTGGTCCCG CTTCTCTTGA GAGCAGGGCA GGGTGGGAACC
 CAGCCTCGCT CCTCCTCAGG GGCTGGAATG GAAGCCAGAG AACAG

22_060 135
 GAAGCAG CCCCAGCATC AGGGACAGGC CAGGAGTGCA GAATGCATGG
 AAGCTGGTCA GGTCGGAGCC
 C/T
 GGGATGAAGG AAGCACAGAG ATGCAAGGGT GCCAGGGCCC ATGGAACCAA
 GAGCCGATGA TCAAGGC

22_062 144

CTT GCCACATTGC TTGGATGGCC TTTCACCAGG TCTGATCCGA GGGTGGTCTC
 G/A
 TCTTTGTCTT AGCAGCCGAG GTCTGTGACC TTGACCACCT GGTGAAGTGT
 TTGCTGTAAA GTCACTCTTT TTTCCTTGCT TCCCATACTG

22_064 112
 AGT GGTGTGATCA TAGCTCACTG CAGCCTCGTC CTCCTGAGCT
 CAGCTGATCC TCCAGCCTCA
 G/A
 CCTCTGAGT GGCTGAGACT ATATGTGTAC ACCAGCATGC CTGGCTAA

22_065 112
 GACTGG GATGGGCAAG AGGTACGGGA CCTGCTCGGC TCACCTCCCT
 C/T
 CTGCAGAGAG ACTCCCAAGG GCTCAGCTGC TCAGAACACT CTAGTTGCCC
 GTGAGGAGCC CAGGG

22_066 138
 TGCAAAGAC ACAATAAGCT ACGTATACAT AGTGGTATAC ATATGCACGC
 ACATACATGC AC
 A/G
 TCCACAATCC ATGTTCTAT GCACCTGTTT CTGCCCATGC AGGTTCATGC
 ACACATATTC CCTGCAAATG TTTGTC

22_067 147
 GTGAATGGAG ATGGACACAT AGCCCTGGGG TAGTTGGAGC TTTTCCTGGC
 A/G
 GTATCCATGG CAACAGGAAG CACAAACAGA AGCATCATTC TACAGCCAAC
 AAAGAGTTCG TTTTAAAAAT CACCATTATC TTTTCAGAGT GCTTCT

22_068 135
 AAGGGCTGAG AGAACTAGAA GAGCCTGATA AGGATCTGGA GAAGAGGCAG
 CTTCCGACCT TTGATGCCAC AGTCACTCTG
 C/T
 GCTACACCTT CATGCAGGGT CCATGCTGTG GCTGATTTC CAGAGTGGGA
 TATT

22_069 145
 TGGCTCAGTT GCCTGCTTGA GGGGATATTT GTGTCTGTCC CTCATACC
 A/G
 GCCACACAAA CCTCCTCAGC CTGGACCACA TGCACGGGTG ACTCCTAGAT
 CCCTATCTTT GACCTCCATG CCTAGGCACC TGGCATCTTC CAGCAT